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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:57:04 ; Search time 46.9787 Seconds
(without alignments)
292.376 Million cell updates/sec

Title: US-10-077-438-1
Perfect score: 964
Sequence: 1 MLQAGCQSQNEVFDLSLHA.....CKSLPAALSATIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	4	US-09-565-423-11
2	964	100.0	192	4	US-09-949-016-11115
3	950	98.5	181	4	US-09-854-864-5
4	572	59.3	185	4	US-09-565-423-17
5	572	59.3	185	4	US-09-854-864-11
6	323	33.5	58	4	US-09-854-864-21
7	311.5	32.3	117	4	US-09-854-864-12
8	286	29.7	283	4	US-09-854-864-9
9	284	29.5	51	4	US-09-854-864-6
10	201	20.9	34	4	US-09-854-864-7
11	201	20.9	81	4	US-09-854-864-13
12	187	19.4	281	4	US-09-854-864-10
13	104	10.8	21	4	US-09-854-864-8
14	79.5	8.2	1009	2	US-08-357-642A-1
15	79.5	8.2	1009	2	US-08-460-626-1
16	79.5	8.2	1014	4	US-09-949-016-11533
17	78.5	8.1	293	2	US-08-810-572A-2
18	78.5	8.1	233	3	US-09-290-333-2
19	78.5	8.1	293	4	US-09-782-857A-2
20	78.5	8.1	293	4	US-09-879-919-22
21	78.5	8.1	293	4	US-09-848-295-4
22	78.5	8.1	293	4	US-09-854-864-14
23	76	7.9	744	1	US-08-179-481-2
24	75	7.8	857	1	US-07-717-331F-2
25	73.5	7.6	307	4	US-09-583-110-2671
26	73.5	7.6	312	4	US-09-107-433-2965
27	71.5	7.4	835	4	US-09-489-039A-8740

28	71	7.4	333	4	US-09-328-352-6022	Sequence 6022, Ap
29	70.5	7.3	154	3	US-09-232-160-18	Sequence 18, Appl
30	70.5	7.3	397	4	US-09-854-864-18	Sequence 18, Appl
31	70.5	7.3	467	4	US-09-902-540-11298	Sequence 11298, A
32	70	7.3	180	4	US-09-780-717-11	Sequence 11, Appl
33	70	7.3	182	4	US-09-780-717-44	Sequence 44, Appl
34	69.5	7.2	59	4	US-09-854-864-20	Sequence 20, Appl
35	69.5	7.2	166	2	US-08-810-572A-6	Sequence 6, Appl
36	69.5	7.2	166	3	US-09-290-333-6	Sequence 6, Appl
37	69.5	7.2	166	4	US-09-782-857A-6	Sequence 6, Appl
38	69.5	7.2	166	4	US-09-854-864-15	Sequence 15, Appl
39	69.5	7.2	217	4	US-09-252-991A-30641	Sequence 30641, A
40	69.5	7.2	224	4	US-09-465-901-30	Sequence 30, Appl
41	69.5	7.2	353	4	US-09-328-352-5429	Sequence 5429, Ap
42	69.5	7.2	942	4	US-09-695-481-2	Sequence 2, Appl
43	69.5	7.2	1043	4	US-09-695-481-6	Sequence 6, Appl
44	69.5	7.2	1180	3	US-08-660-148-2	Sequence 2, Appl
45	69.5	7.2	1212	3	US-08-660-148-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match	100.0%;	Score 964;	DB 4;	Length 184;
Best Local Similarity	100.0%;	Pred. NO. 1e-103;		
Matches 184;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLQWAGCQSQNEVFDLSLHACIPQLRCSNSTPPLTCORYCNASVTNSVKGTTNAILWTCL	60	
Db	1	MLQWAGCQSQNEVFDLSLHACIPQLRCSNSTPPLTCORYCNASVTNSVKGTTNAILWTCL	60	
QY	61	GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE	120	
Db	61	GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE	120	
QY	121	YTVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS	180	
Db	121	YTVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS	180	
QY	181	ISAR 184		
Db	181	ISAR 184		

RESULT 2

US-09-949-016-11115
; Sequence 11115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11115
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-11115

Query Match 100.0%; Score 964; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCQNEFYFDSLLHACIPQCLRCSSNTPTTCORYCNASVTNSVKGTHAILWTCL 60
DB 9 MLQAGCQNEFYFDSLLHACIPQCLRCSSNTPTTCORYCNASVTNSVKGTHAILWTCL 68
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGL 120
DB 69 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGL 128
QY 121 YTVBECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
DB 129 YTVBECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 188
QY 181 ISAR 184
DB 189 ISAR 192

RESULT 3
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 98.5%; Score 950; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.3e-102;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCQNEFYFDSLLHACIPQCLRCSSNTPTTCORYCNASVTNSVKGTHAILWTCLGLS 63
DB 1 MAGCQNEFYFDSLLHACIPQCLRCSSNTPTTCORYCNASVTNSVKGTHAILWTCLGLS 60
QY 64 LIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 123

DB 61 LIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 120
QY 124 EECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
DB 121 EECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
QY 184 R 184
DB 181 R 181

RESULT 4
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match 59.3%; Score 572; DB 4; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.3e-58;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGCQNEFYFDSLLHACIPQCLRCSSNTPTTCORYCNASVTNSVKGTHAILWTCLGLS 63
DB 1 MAQCQFHEFYFDSLLHACKCHLRCSN--PPATCQPCDPSVTSSVKGTYYVLMIFLGLT 58
QY 64 LIISLAVFVLMFLRLKISSEPLKDEPKN---TSGLLGMANIDLEKSRGTGDEIILPRGL 119
DB 59 LVLSLALFTISFLLEKMPKALKEPQSGQLDGSQAQDKADTELTRIRAGDRIFPRSL 118
QY 120 EYTVBECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
DB 119 EYTVBECTCEDCKSKPKGSDSHFPPLPAMEEGATILVTTKTGDKSVPTALQSMGM 178
QY 178 EKSISAR 184
DB 179 EKPTHTR 185

RESULT 5
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

```

Query Match 59.3%; Score 572; DB 4; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.3e-58;
Matches 117; Conservative 21; Mismatches 41; Indels

Qy	4	MAGQCSONEYFDFSLHACIPQOLRCSSNTPPLTCQRYCNASVTVNSVKGTTNAILWTCLIGLS	63
Db	1	MAQOCFHSEYFDFSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTTVTLWIFLGLT	58
Qy	64	LIISLAVFLVFLPLLRKISSEPLKOEFKN----TCSGLLGMANTDLEKSRGDEIILIPRGL	119
Db	59	LVLSLALFTISPLLRKMNPEALKOEPOSQGLDGSQQLDKADTELTRIRAGDDRIIFRSL	118
Qy	120	EYTVBEECTCEDCISKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI	177
Db	119	EYTVBEECTCDVSKPKGSDSDHFPPLPAMEEGATILVTTKTDYCKGSSVPTALQSVGM	178
Qy	178	EKSISAR	184
Db	179	ERPTTHR	185

RESULT 6
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/ACP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match	33.5%	Score 323;	DB 4;	Length 58;
Best Local Similarity	100.0%;	Prod. No. 5e-30;		
Matches	58;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	8	CSONEYFDSLHLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGNTAILWTCLGSLI	65	
Db	1	CSONEYFDSLHLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGNTAILWTCLGSLI	58	

RESULT 7
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11

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; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
; US-09-854-864-12

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	Query Match	32.3%	Score 311.5;	DB 4;	Length 117;
	Best Local	Similarity 61.5%;	Pred. No. 2.9e-28;		
	Matches	96;	Conservative 4;	Mismatches 7;	Indels 49; Gaps 19;
Qy	9	SONEYDLSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNALIWTCLGLSLIISL	68		
Db	2	AQCEYFDLSLHAC-PC-LRCS-----PPTCO-YC--SVT-SVKGT--LW--LGL---LSL	43		
Qy	69	AVFVLFLLRKISSEPLKDEFKFTGSGLLGMANIDLEKSRITGDBIIILPRGLEYYTVECTC	128		
Db	44	A-----FLLRK-----ELKDE-----GSLAL-----RGD---IPR-LEYTVECTC	76		
Qy	129	EDCIKSKPKVDSHCPPLPAMEGATILVTTKNDY	164		
Db	77	EDC-KSKPK-DSOH-FPLPAMEGATILVTTKY-DY	108		

RESULT 8
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 674106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

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Query Match      29.7%; Score 286; DB 4; Length 283;
Best Local Similarity 37.6%; Pred. No. 9.4e-25;
Matches      80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

QY      4  MAGQCSQNEYFDSLLHACIPCOLRCSNSTPPLTCQRYCNASVTSVSKGTNAILWTCGLS 63
         |||||
Db       1  MAGQCSQNEYFDSLLHACIPCOLRCSNSTPPLTCQRYCNASVTSVSKGTNA----- 51

QY      64  LIISLAVFMFLRLKRISSEPLKDEPKNTGSG-----LLGMNIDLEKSRGT 110
         ||| :|
Db       52  -----GGGGGDKHTTCCPCAPELGGPSVFLFPKPK 84

QY      111  DEIILPRGLETVVEECTCBDCIKSKPKVDS-----HCFPLPAMEE-----GATIL 156
         ||| :|
Db       85  DTLMISETPEVT---CWVDVSHEDPEVFNWYDGVGHVNAKTPREEQYNSTYRVSV 141

QY      157  VTTKTDNY-----CKSLPAALGATELEKSI 182

Db      142  LTVLHODWLNGREYKCKVSNKALPA-PIEKTIS 173

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RESULT 9
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 29.5%; Score 284; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGCCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKGNA 54
Db 1 MAGCCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKGNA 51

RESULT 10
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 20.9%; Score 201; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 11
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 20.9%; Score 201; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 12
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 19.4%; Score 187; DB 4; Length 281;
Best Local Similarity 29.8%; Pred. No. 2.9e-13;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;
QY 4 MAGCCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKGNAITWTCGLS 63
Db 1 MAQCQFHSSEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKGNAITWTCGLS 47
QY 64 LIISLAVFVLMFLRKISSEPLKDEPKNTGSG-----LLGMANIDLEKSR 108
Db 48 -----YTGCGGDKTKHTCPCPAPELLGSGSVFLFPPK 80
QY 109 TGDRIILPRGLETVVECTCEDCIKSKPKVDS-----HCFPLPAMEE-----GAT 154
Db 81 PKDTLMISRTPEVT---CVVDVSHEDPEVKFNWYDGVFVHNAKTKPREQYNSTRV 137
QY 155 ILVTTKTNDY-----CKSLPAALSATEIEKSTIS 182
Db 138 SVLTVLHQDWLNGEYKCKVSNKALPA-PIEKTIS 171

RESULT 13

```
US-09-854-864-8
; Sequence 8, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-8

Query Match      10.8%; Score 104; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 ILWTCGLSLIISLAVFLVLMF 75
Db 1 ILWTCGLSLIISLAVFLVLMF 21

RESULT 14
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-626-1
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; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-357-642A-1

Query Match      8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5.4;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLETVBECTCEDICKPKV 138
Db 249 KFFNT---LAGFANIDQETRCBELIQGWNITVDLVIGPKGIQRLTSDAKPTCLAEFKQI 305
QY 139 DSDHCFPLPAMEEGATIL 156
Db 306 RSIRCLPL---EGQAVL 320

RESULT 15
US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-626-1

Query Match      8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5.4;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLETVBECTCEDICKPKV 138
```

Db 249 KPENT--LAGFANIDQETVRCELIQGNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
QY 139 DSDHCFPLPAMEGATIL 156
Db 306 RSIRCLPL---BEGQAVL 320

Search completed: February 26, 2005, 21:06:28
Job time : 47.9787 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:24:52 ; Search time 194.962 Seconds
(without alignments)
365.015 Million cell updates/sec

Title: US-10-077-438-1
Perfect score: 964
Sequence: 1 MLOMACQSQNEVDFSLHA.....CKSLPAALGATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	3 AAB08843	Aab08843 Amino aci
2	964	100.0	184	3 AAY94001	Aay94001 A human B
3	964	100.0	184	4 AAE09241	Aae09241 Human BCM
4	964	100.0	184	4 AAY71979	Aay71979 Human B c
5	964	100.0	184	4 AAB60698	Aab60698 Human BAF
6	964	100.0	184	4 AAE00506	Aae00506 Human B c
7	964	100.0	184	5 ABB81487	Abb81487 Human BCM
8	964	100.0	184	5 ABP54694	Abp54694 Metastati
9	964	100.0	184	5 AAE28961	Aae28961 Human B-c
10	964	100.0	184	5 AAE35216	Aae35216 Human B-c
11	964	100.0	184	6 ADA49361	Ada49361 Human BCM
12	964	100.0	184	6 ABP60552	Abp60552 Human tum
13	964	100.0	184	6 ABP97717	Abp97717 Amino aci
14	964	100.0	184	7 ADD67527	Add67527 Human Lyl
15	964	100.0	184	7 ADG43715	Adg43715 Human B-c
16	964	100.0	184	8 ADK00756	Adk00756 Native hu
17	964	100.0	184	8 ADQ94442	Adq94442 Neutrokin
18	964	100.0	184	8 ADP56014	Adp56014 Human PRO
19	958	99.4	184	6 ABR40082	Abra40082 Human Gen
20	955	99.1	288	5 ABG95060	Abg95060 Human tra
21	950	98.5	181	5 AAE15484	Aae15484 Human B-c
22	719.5	74.6	157	4 AAB60700	Aab60700 Human BAF
23	572	59.3	185	3 AAB08844	Aab08844 Amino aci
24	572	59.3	185	4 AAY71980	Aay71980 Murine B
25	572	59.3	185	5 AAE15490	Aae15490 Mouse B c

26	323	33.5	58	5	AAE15501	Aae15501 Human B c
27	311.5	32.3	117	5	AAE15491	Aae15491 Human-mur
28	286.5	29.7	302	4	AAB60699	Aab60699 Mouse IGG
29	286.5	29.7	302	4	AAE00507	Aae00507 Human BCM
30	286.5	29.7	302	7	ADG43717	Adg43717 Human B-c
31	286	29.7	283	5	AAE15488	Aae15488 Human BCM
32	284	29.5	51	5	AAE15485	Aae15485 Human B-c
33	201	20.9	34	5	AAE15486	Aae15486 Human B-c
34	201	20.9	34	6	ADA49366	Ada49366 Human BCM
35	187	19.4	281	5	AAE15489	Aae15489 Mouse BCM
36	158	16.4	42	6	ABJ38417	Abj38417 TALL-1 re
37	151	15.7	26	7	ADI3060	Adi3060 Human BCM
38	116.5	12.1	175	5	ABB78398	Abb78398 Amino aci
39	116.5	12.1	175	5	AAE22244	Aae22244 Murine BA
40	116.5	12.1	175	5	ABB81489	Abb81489 Mouse Ztn
41	116.5	12.1	175	6	ABP97722	Abp97722 Amino aci
42	106.5	11.0	185	5	AAE22266	Aae22266 Human BAF
43	105.5	10.9	185	5	AAE22267	Aae22267 Human BAF
44	104	10.8	21	5	AAE15487	Aae15487 Human B-c
45	103.5	10.7	185	5	AAE22269	Aae22269 Human BAF

ALIGNMENTS

RESULT 1
AAB08843
ID AAB08843 standard; peptide; 184 AA.
AC AAB08843;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of human.
XX
KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 57..77
FT /note= "putative transmembrane domain"
XX
PN WO200050633-A1.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-US004925.
XX
PR 24-FEB-1999; 99US-0121485P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Ting A;
XX
WPI; 2000-558405/51.
PT Identifying a modulator of gene expression for drug designing, by
PT contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
XX expression.
PS Claim 32; Fig 7A; 53pp; English.
XX

The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to

CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIISLAVFLVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 DB 61 GLSLIISLAVFLVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 2
 AAY94001
 ID AAY94001 standard; protein; 184 AA.
 AC AAY94001;
 XX
 XX 20-OCT-2000 (first entry)
 DE
 XX A human BCMA protein, a B cell protein related to TACI.
 XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 XX Homo sapiens.
 XX
 XX WO200040716-A2.
 XX
 XX 13-JUL-2000.
 XX
 XX 07-JAN-2000; 2000WO-US000396.
 XX
 XX 07-JAN-1999; 99US-00226533.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Madden K, Yee DP;
 XX
 XX WPI; 2000-452538/39.
 XX
 XX N-PSDB; AAA56559.
 XX
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 XX
 XX

PT renal disease, graft versus host disease, and inflammation, comprises
 XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX
 XX Disclosure; Page 152; 175pp; English.

The present sequence represents a human BCMA protein, a B cell protein
 related to transmembrane activator and CAML-interactor (TACI) receptor.
 TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIISLAVFLVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 DB 61 GLSLIISLAVFLVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 3
 AAE09241
 ID AAE09241 standard; protein; 184 AA.

XX AAE09241;
 XX
 XX 19-NOV-2001 (first entry)
 XX
 XX Human BCMA protein.
 XX
 XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 XX
 XX Homo sapiens.
 XX
 XX WO200160397-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 28-NOV-2000; 2000WO-US032378.
 XX
 XX 16-FEB-2000; 2000US-0182938P.
 XX

PR 22-AUG-2000; 2000US-0226986P.
PA (GETH) GENENTECH INC.
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM,
PI Yan M;
XX WPI; 2001-541628/60.
DR N-PSDB; AAD15902.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.
XX
XX Example 2; Fig 2; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
XX TACI or BCMA. The method is useful for treating pathological conditions
XX or diseases associated with increased TALL-1 and APRIL expression or
XX activity. TALL-1 and APRIL antagonists are used to block the interaction
XX between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
XX a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
XX cancers of lung and colon and autoimmune diseases e.g. rheumatoid
XX arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
XX present sequence is human BCMA protein
XX
XX Sequence 184 AA;
XX
Query Match 100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MLQWAGQCSQNEYFDSLLHACIPQLRCSSTNPTPLTCQRYCNASVTSVKGTTNAILWTCL 60
DB 1 MLQWAGQCSQNEYFDSLLHACIPQLRCSSTNPTPLTCQRYCNASVTSVKGTTNAILWTCL 60
XX
QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
DB 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
XX
QY 121 YTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
DB 121 YTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
XX
QY 181 ISAR 184
DB 181 ISAR 184
XX
RESULT 4
AAV71979
ID AAV71979 standard; protein; 184 AA.
XX
AC AAV71979;
XX
XX 28-MAR-2001 (first entry)
DT
XX Human B cell maturation factor (BCMA) protein.
DE
XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
XX B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX Homo sapiens.
XX

PH Key Location/Qualifiers
FT Domain 1..62
XX /label= Extracellular_domain
XX WO200068378-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US012266.
XX
XX 06-MAY-1999; 99US-0132892P.
XX 01-MAY-2000; 2000US-0201012P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Shu HS;
XX
XX WPI; 2001-016094/02.
XX N-PSDB; AAD02125.
XX
XX Isolated TALL-1 protein is used to identify compounds that regulate B
XX lymphocyte proliferation, used to treat B lymphocyte associated
XX autoimmune disorders.
XX
XX Claim 37; Page 104-105; 112pp; English.
XX
XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
XX related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
XX proteins (including homologues), and their antibodies. The invention in
XX particular relates to methods for regulating the interaction between TALL
XX -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
XX regulate monocyte, macrophage and B lymphocyte mediated immune responses.
XX TALL-1 protein is useful for identifying compounds that regulate B
XX lymphocyte proliferation. It is also useful for treating B lymphocyte
XX associated autoimmune disorders like rheumatoid arthritis, systemic lupus
XX erythematosus (SLE), insulin dependent diabetes mellitus, multiple
XX sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
XX pemphigus vulgaris, acute rheumatic fever, post-streptococcal
XX glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
XX corresponding nucleic acid sequence are also useful in diagnostic assays.
XX The present sequence is a human B cell maturation factor (BCMA) protein.
XX It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
XX 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
XX by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
XX BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
XX increases with B lymphocyte maturation
XX
XX Sequence 184 AA;
XX
Query Match 100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MLQWAGQCSQNEYFDSLLHACIPQLRCSSTNPTPLTCQRYCNASVTSVKGTTNAILWTCL 60
DB 1 MLQWAGQCSQNEYFDSLLHACIPQLRCSSTNPTPLTCQRYCNASVTSVKGTTNAILWTCL 60
XX
QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
DB 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
XX
QY 121 YTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
DB 121 YTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
XX
QY 181 ISAR 184
DB 181 ISAR 184
XX
RESULT 5
AAB60698

CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is human APRIL-R also referred as BCM or BCM protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCCSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 DB 1 MLQAGCCSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRLKISSBPLKDEFKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLRLKISSBPLKDEFKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
 QY 121 YTVECTCEDCIKSPKVDSDHCFFPLPAMEEGATILVTTKNDYCKSLPALSAITEKS 180
 DB 121 YTVECTCEDCIKSPKVDSDHCFFPLPAMEEGATILVTTKNDYCKSLPALSAITEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 7
 ABB81487
 ID ABB81487 standard; protein; 184 AA.
 XX
 AC ABB81487;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Human BCMA receptor related protein SEQ ID NO:7.
 XX

KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX

OS Homo sapiens.
 XX
 XX WO200238766-A2.
 XX
 PD 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US047018.
 XX
 XX 07-NOV-2000; 2000US-0246449P.
 PR 20-DEC-2000; 2000US-0257131P.
 PR 28-JUN-2001; 2001US-0301715P.
 PR 29-AUG-2001; 2001US-0315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 PI
 XX WPI; 2002-508212/54.
 DR
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed

PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.
 XX
 PS Disclosure; Page 135-136; 154pp; English.
 XX

CC The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCCSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 DB 1 MLQAGCCSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRLKISSBPLKDEFKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLRLKISSBPLKDEFKNTGSLGGMANIDLEKSRGTDEILPRGLE 120
 QY 121 YTVECTCEDCIKSPKVDSDHCFFPLPAMEEGATILVTTKNDYCKSLPALSAITEKS 180
 DB 121 YTVECTCEDCIKSPKVDSDHCFFPLPAMEEGATILVTTKNDYCKSLPALSAITEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 8
 ABP54694
 ID ABP54694 standard; protein; 184 AA.
 XX
 AC ABP54694;
 XX

DT 30-DEC-2002 (first entry)
 XX
 XX Metastatic colorectal cancer-associated polypeptide.
 XX
 XX Colorectal cancer; metastasis; differential expression; cytostatic;
 KW diagnosis; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX WO200268677-A2.
 XX
 XX 06-SEP-2002.
 XX
 XX 27-FEB-2002; 2002WO-US006001.
 PF
 XX 27-FEB-2001; 2001US-0272206P.
 PR

PR 02-APR-2001; 2001US-0281149P.
 PR 17-APR-2001; 2001US-0284555P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX Mack DH, Markowitz SD;
 XX PI
 XX WPI; 2002-598677/75.
 DR N-PSDB; ABQ81560.
 DR
 XX New genes that are up- or down-regulated in colorectal cancer, useful for
 PT diagnosing colorectal cancer in a subject, or for identifying modulators
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.
 XX
 PS Claim 8; Page 255; 260pp; English.
 XX
 CC The present sequence is the protein sequence of a human polypeptide
 CC encoded by a gene that exhibits decreased expression in colon cancer-
 CC derived metastases compared to normal colon tissue. It is an example of
 CC claimed polypeptides that are encoded by genes which are differentially
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are
 CC useful in diagnostic and prognostic assays, for raising antibodies useful
 CC e.g. in immunotherapy, and in screening for modulator compounds of
 CC therapeutic value
 CC
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 QY 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 9
 AAE28961
 ID AAE28961 standard; protein; 184 AA.
 XX AC
 XX AAE28961;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Human B-cell maturation antigen (BCMA).
 XX
 KW Human; tumour; B-cell maturation antigen; transmembrane activator;
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 KW BCMA; multiple myeloma.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..54
 FT /note= "Antigenic epitope"
 FT 1..48
 FT /note= "Extracellular domain"

FT Region 8..41
 FT /note= "Cysteine rich. region"
 XX
 PN WO200266516-A2.
 XX
 XX 29-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-US003500.
 XX
 XX 20-FEB-2001; 2001US-0270274P.
 PR 12-APR-2001; 2001US-0283447P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Kindsvogel W;
 XX
 XX WPI; 2002-723183/78.
 DR N-PSDB; AAD46410.
 DR
 XX B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.
 XX
 PS Disclosure; Page 63; 67pp; English.
 XX
 CC The invention relates to the manufacture of a composition for inhibiting
 CC the proliferation of tumour cells. The method involves using an antibody
 CC component that binds both the B-cell maturation antigen (BCMA) and the
 CC transmembrane activator and calcium-modulator and cyclophilin ligand-
 CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
 CC for inhibiting proliferation of tumour cells, particularly inhibiting
 CC ZTNF4 activity in a mammal associated with increased endogenous antibody
 CC production or a disorder consisting of neoplasm, chronic lymphocytic
 CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
 CC lymphoproliferative disease or light chain gammopathy or inflammation
 CC e.g. asthma. The invention is also useful in gene therapy. The present is
 CC human BCMA protein
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
 QY 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 10
 AAE35216
 ID AAE35216 standard; protein; 184 AA.
 XX AC
 XX AAE35216;
 XX
 XX 28-MAY-2003 (first entry)
 DT
 XX Human B-cell maturation receptor (BCMA) protein.
 DE
 XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;

KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW B-cell maturation receptor; BCMA; receptor.
 XX Homo sapiens.
 OS
 XX WO200294852-A2.
 PN
 XX
 XX
 XX 28-NOV-2002.
 PD
 XX
 XX 20-MAY-2002; 2002WO-US015910.
 PF
 XX
 XX 24-MAY-2001; 2001US-0293343P.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Rixon MW, Gross JA;
 PI
 XX
 XX WPI; 2003-148455/14.
 DR
 XX N-PSDB; ADA53754.
 DR
 XX
 XX Transmembrane activator and calcium modulator and cyclophilin ligand-
 PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
 PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
 PT
 XX
 XX Disclosure; Col 100; 71pp; English.
 PS
 XX
 XX The invention relates to fusion proteins comprising transmembrane
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an
 CC immunoglobulin. The invention is used to manufacture a medicament for
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The
 CC composition comprising the fusion protein may also be used in treating
 CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
 CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
 CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
 CC rejection, anaemia and septic shock. The fusion proteins are also used in
 CC gene therapy. The present sequence is human B-cell maturation receptor
 CC (BCMA) protein used in the invention
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPQQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
 Db 1 MLQAGQCSQNEYFDSLHACIPQQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 Db 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 QY 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
 Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184
 RESULT 11
 ADA49361
 ID ADA49361 standard; protein; 184 AA.
 XX
 AC ADA49361;
 XX

DT 20-NOV-2003 (first entry)
 XX Human BCMA protein.
 DE
 XX human; TALL-1; antagonist; immunosuppressive; anti-rheumatic;
 KW antiinflammatory; antiarthritic; dermatological; antidiabetic;
 KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
 KW vaccine; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
 KW multiple sclerosis; myasthenia gravis; Grave's disease;
 KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
 KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
 XX Homo sapiens.
 OS
 XX WO2003035846-A2.
 PN
 XX
 XX 01-MAY-2003.
 PD
 XX
 XX 24-OCT-2002; 2002WO-US034376.
 PF
 XX
 XX 24-OCT-2001; 2001US-0345106P.
 PR
 XX 14-JAN-2002; 2002US-0348962P.
 PR
 XX 07-FEB-2002; 2002US-0354966P.
 PR
 XX 13-AUG-2002; 2002US-0403364P.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 PA
 XX
 XX Zhang G, Shu H, Liu Y, Xu L;
 PI
 XX
 XX WPI; 2003-403345/38.
 DR
 XX N-PSDB; ADA49360.
 DR
 XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.
 PT
 XX Claim 62; Page 613; 618pp; English.
 PS
 XX The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting 4bgr; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, anti-rheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFDSLHACIPQQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
 Db 1 MLQAGQCSQNEYFDSLHACIPQQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 Db 61 GLSLIISLAVFVLMFLRLKISSSEPLKDFPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 QY 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

Db 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184

RESULT 12
 ABP60552
 ID ABP60552 standard; protein; 184 AA.
 XX
 AC ABP60552;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Human tumour necrosis factor BCMA.
 XX
 KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; anti-inflammatory; antirheumatic;
 KW antarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic;
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200294192-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 22-MAY-2002; 2002WO-US016106.
 XX
 PR 24-MAY-2001; 2001US-0293100P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM;
 XX
 XX WPI; 2003-156740/15.
 DR
 XX
 PT Novel isolated antibody that immunospecifically binds tumor necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.
 PS
 PS Disclosure; Page 222; 225pp; English.
 XX
 CC The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC anti-inflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,
 CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents

CC the tumour necrosis factor BCMA
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
 Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
 QY 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSLGLGWANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSLGLGWANIDLEKSTGDEIILPRGLE 120
 QY 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 QY 181 ISAR 184
 Db 181 ISAR 184

RESULT 13
 ABP97717
 ID ABP97717 standard; protein; 184 AA.
 XX
 AC ABP97717;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Amino acid sequence of human BCMA receptor.
 XX
 KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus; BCMA.
 XX
 OS Homo sapiens.
 XX
 PN WO2003014294-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 24-JUL-2002; 2002WO-US023487.
 XX
 PR 03-AUG-2001; 2001US-0310114P.
 PR 30-APR-2002; 2002US-0377171P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dixit V, Grewal I, Ridgway J, Yan M;
 XX
 DR WPI; 2003-256560/25.
 DR N-P8DB; ABZ68871.
 XX
 PT New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.
 XX
 PS Disclosure; Fig 2; 153pp; English.
 XX
 CC The present sequence represents a human BCMA polypeptide. The
 CC specification also describes TAC1 and BR3 polypeptides. TAC1 and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVNSVKGNTNAILWTCL 60
 DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVNSVKGNTNAILWTCL 60
 QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 DB 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120
 QY 121 YTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
 DB 121 YTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 14

ADD67527
 ID ADD67527 standard; protein; 184 AA.

XX AC ADD67527;

DT 15-JAN-2004 (first entry)

XX DE Human Ly1732P protein SEQ ID NO:4.

XX KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
 KW vaccine; immunotherapy; cancer; multiple myeloma cell;
 KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
 KW human.

XX OS Homo sapiens.

XX PN WO2003062401-A2.

XX PD 31-JUL-2003.

XX PF 22-JAN-2003; 2003WO-US002353.

XX PR 22-JAN-2002; 2002US-00057475.

XX PA (CORI-) CORIXA CORP.

XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
 PI Carter L, McNeill PD;

XX WPI; 2003-598749/56.

XX DR N-PSDB; ADD67526.

XX PT New hematological malignancy-related genes and polypeptides, useful for
 PT screening anti-cancer agents, and generating antibodies or
 PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
 PT lymphocytic leukemia.

PS Claim 9; SEQ ID NO 4; 307pp; English.

XX CC The present invention describes an isolated polynucleotide (I), which is
 CC overexpressed in haematological malignancies, and which encodes a
 CC polypeptide or an immunogenic fragment of the polypeptide. Also
 CC described: (1) an isolated polypeptide; (2) an expression vector
 CC comprising (1) operably linked to an expression control sequence; (3) a
 CC host cell comprising an expression vector; (4) an isolated antibody that
 CC specifically binds to the polypeptide or its immunogenic fragment; and
 CC (5) immunoconjugates comprising the antibody above, or an antibody that
 CC specifically binds to a polypeptide, or its immunogenic fragment, and can be
 CC by (1). (I) has cytostatic and immunostimulant activities, and can be
 CC used in vaccines and immunotherapy. The immunoconjugates are useful in
 CC the manufacture of a medicament, particularly as active ingredients in a
 CC composition for treating cancer, e.g. multiple myeloma cell, chronic
 CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
 CC primates, goats, bovines, equines, porcines, lupines, canines or felines.

CC The polynucleotide (I) or polypeptide can be used for screening anti-
 CC cancer agents, and generating antibodies or immunoconjugates for treating
 CC or preventing the above-mentioned diseases. The polynucleotide,
 CC polypeptide or antibody can be used for detecting, diagnosing or
 CC prognosticating the haematological malignancies described above. The
 CC present sequence is used in the exemplification of the present invention.
 XX Sequence 184 AA;

Query Match 100.0%; Score 964; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVNSVKGNTNAILWTCL 60

DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVNSVKGNTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120

DB 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

DB 121 YTVVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

QY 181 ISAR 184

DB 181 ISAR 184

RESULT 15

ADG43715
 ID ADG43715 standard; protein; 184 AA.

XX AC ADG43715;

DT 26-FEB-2004 (first entry)

XX DE Human B-cell maturation antigen SEQ ID NO:1.

XX KW human; neurodegenerative immunological disorder; demyelination;
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
 KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
 KW gene therapy.

XX OS Homo sapiens.

XX PN WO2003072713-A2.

XX PD 04-SEP-2003.

XX PF 21-FEB-2003; 2003WO-US005147.

XX PR 21-FEB-2002; 2002US-0358427P.

XX PA (BIOJ) BIOGEN INC.

XX PI Kalled SL, Reid H;

XX WPI; 2003-721758/68.

XX DR N-PSDB; ADG43716.

XX PT Treating a neurodegenerative immunological disorder, e.g. demyelination
 PT or inflammation in a mammal comprises administering a B-cell maturation
 PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

PS Claim 8; Page 68-69; 72pp; English.

XX CC The invention relates to a novel method for treating a neurodegenerative
 CC immunological disorder, demyelination or Central Nervous System (CNS)
 CC inflammation in a mammal. The method comprises administering B-cell
 CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
 CC (the mammal has or is at risk of developing multiple sclerosis). The

CC method of the invention has neuroprotective, nootropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence represents human BCMA.

XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGQCSQNEYFDSLLHACIPQLCRCSSNTPTPTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLLHACIPQLCRCSSNTPTPTCQRYCNASVTNSVKGTHAILWTCL 60
QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

Search completed: February 26, 2005, 20:45:21
Job time : 197.962 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 20:41:13 ; Search time 139.37 Seconds
(without alignments)
433.092 Million cell updates/sec

Title: US-10-077-438-1

Perfect score: 964

Sequence: 1 MLQAGQCSQNEFYDFSLHA.....CKSLPAALSATBIKSIAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	964	100.0	184	13 US-10-077-438-1	Sequence 1, Appli
2	964	100.0	184	13 US-10-077-438-7	Sequence 7, Appli
3	964	100.0	184	13 US-10-077-137-1	Sequence 1, Appli
4	964	100.0	184	13 US-10-077-137-7	Sequence 7, Appli
5	964	100.0	184	14 US-10-068-725-2	Sequence 2, Appli
6	964	100.0	184	14 US-10-151-882-47	Sequence 47, Appli
7	964	100.0	184	14 US-10-115-192-8	Sequence 8, Appli
8	964	100.0	184	14 US-10-008-063-7	Sequence 7, Appli
9	964	100.0	184	14 US-10-152-363A-27	Sequence 27, Appl
10	964	100.0	184	14 US-10-216-074-11	Sequence 11, Appl
11	964	100.0	184	15 US-10-087-080-39	Sequence 39, Appl
12	950	98.5	181	9 US-09-854-864-5	Sequence 5, Appli
13	950	98.5	181	9 US-09-855-158-5	Sequence 5, Appli

14	572	59.3	185	9 US-09-854-864-11	Sequence 11, Appl
15	572	59.3	185	9 US-09-855-158-11	Sequence 11, Appl
16	572	59.3	185	14 US-10-216-074-17	Sequence 17, Appl
17	323	33.5	58	9 US-09-854-864-21	Sequence 21, Appl
18	323	33.5	58	9 US-09-855-158-21	Sequence 21, Appl
19	311.5	32.3	117	9 US-09-854-864-12	Sequence 12, Appl
20	311.5	32.3	117	9 US-09-855-158-12	Sequence 12, Appl
21	286.5	29.7	302	14 US-10-115-192-12	Sequence 12, Appl
22	286	29.7	283	9 US-09-854-864-9	Sequence 9, Appli
23	286	29.7	283	9 US-09-855-158-9	Sequence 9, Appli
24	284	29.5	51	9 US-09-854-864-6	Sequence 6, Appli
25	284	29.5	51	9 US-09-855-158-6	Sequence 6, Appli
26	264	27.4	207	13 US-10-077-438-3	Sequence 3, Appli
27	264	27.4	207	13 US-10-077-137-3	Sequence 3, Appli
28	201	20.9	34	9 US-09-854-864-7	Sequence 7, Appli
29	201	20.9	34	9 US-09-855-158-7	Sequence 7, Appli
30	201	20.9	81	9 US-09-854-864-13	Sequence 13, Appl
31	201	20.9	81	9 US-09-855-158-13	Sequence 13, Appl
32	187	19.4	281	9 US-09-854-864-10	Sequence 10, Appl
33	187	19.4	281	9 US-09-855-158-10	Sequence 10, Appl
34	158	16.4	42	14 US-10-145-206-197	Sequence 197, App
35	116.5	12.1	175	14 US-10-008-063-13	Sequence 13, Appl
36	116.5	12.1	175	15 US-10-380-703-9	Sequence 9, Appli
37	116.5	12.1	175	16 US-10-463-420-1	Sequence 1, Appli
38	104	10.8	21	9 US-09-854-864-8	Sequence 8, Appli
39	104	10.8	21	9 US-09-855-158-8	Sequence 8, Appli
40	100	10.4	185	14 US-10-251-947-2	Sequence 2, Appli
41	94.5	9.8	185	15 US-10-380-703-5	Sequence 5, Appli
42	93	9.6	184	13 US-10-087-192-984	Sequence 984, App
43	93	9.6	184	14 US-10-008-063-2	Sequence 2, Appli
44	93	9.6	184	14 US-10-152-363A-60	Sequence 60, Appl
45	93	9.6	184	15 US-10-380-703-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 QY 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 Db 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 QY 181 ISAR 184
 |||||
 Db 181 ISAR 184
 |||||

RESULT 2

US-10-077-438-7

; Sequence 7, Application US/10077438

; Publication No. US20020165156A1

; GENERAL INFORMATION:

; APPLICANT: Mackay, Fabienne

; APPLICANT: Browning, Jeffrey

; APPLICANT: Ambrose, Christine

; APPLICANT: Tschopp, Jurg

; APPLICANT: Schneider, Pascal

; APPLICANT: Thompson, Jeffrey

; APPLICANT: Biogen, Inc.

; APPLICANT: Apotech R&D S.A.

; TITLE OF INVENTION: Baff Receptor (BCMA), An

; FILE REFERENCE: A080PCT

; CURRENT APPLICATION NUMBER: US/10/077,438

; PRIOR FILING DATE: 2002-02-18

; PRIOR APPLICATION NUMBER: 60/149,378

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/181,684

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 60/183,536

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 184

; TYPE: PRT

; ORGANISM: homo sapien

US-10-077-438-7

Query Match 100.0%; Score 964; DB 13; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 QY 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 Db 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 QY 181 ISAR 184
 |||||
 Db 181 ISAR 184
 |||||

RESULT 3

US-10-077-137-1

; Sequence 1, Application US/10077137

; Publication No. US20020172674A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mackay, Fabienne
 ; APPLICANT: Browning, Jeffrey
 ; APPLICANT: Ambrose, Christine
 ; APPLICANT: Tschopp, Jurg
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Thompson, Jeffrey
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Apotech R&D S.A.
 ; TITLE OF INVENTION: Baff Receptor (BCMA), An
 ; FILE REFERENCE: A080PCT
 ; CURRENT APPLICATION NUMBER: US/10/077,137
 ; CURRENT FILING DATE: 2001-02-15
 ; PRIOR APPLICATION NUMBER: 60/149,378
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/181,684
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/183,536
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 US-10-077-137-1

Query Match 100.0%; Score 964; DB 13; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTAIILWTCL 60
 |||||
 QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 QY 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 Db 121 YVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 QY 181 ISAR 184
 |||||
 Db 181 ISAR 184
 |||||

RESULT 4

US-10-077-137-7

; Sequence 7, Application US/10077137

; Publication No. US20020172674A1

; GENERAL INFORMATION:

; APPLICANT: Mackay, Fabienne

; APPLICANT: Browning, Jeffrey

; APPLICANT: Ambrose, Christine

; APPLICANT: Tschopp, Jurg

; APPLICANT: Schneider, Pascal

; APPLICANT: Thompson, Jeffrey

; APPLICANT: Biogen, Inc.

; APPLICANT: Apotech R&D S.A.

; TITLE OF INVENTION: Baff Receptor (BCMA), An

; FILE REFERENCE: A080PCT

; CURRENT APPLICATION NUMBER: US/10/077,137

; CURRENT FILING DATE: 2001-02-15

; PRIOR APPLICATION NUMBER: 60/149,378

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/181,684

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 60/183,536

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; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

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Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
Db 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

QY 181 ISAR 184
Db 181 ISAR 184

RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

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Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
Db 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
Db 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

QY 181 ISAR 184
Db 181 ISAR 184
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RESULT 6
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match      100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
Db 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180
Db 121 YTVVECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATIEKS 180

QY 181 ISAR 184
Db 181 ISAR 184

RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
Db 1 MLQAGCCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTSVKGTTNAILWTCL 60
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```
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184
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RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7
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Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184
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RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184
```

```
RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US2003014845A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11
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Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60
QY 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184
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```
RESULT 11
US-10-087-080-39
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; Sequence 39, Application US/10087080
; Publication No. US20030235820A1

GENERAL INFORMATION:

; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.

; APPLICANT: Case Western Reserve University

; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

; FILE REFERENCE: 018501-000840US

; CURRENT APPLICATION NUMBER: US/10/087,080

; CURRENT FILING DATE: 2002-10-25

; PRIOR APPLICATION NUMBER: US 60/272,206

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 60/281,149

; PRIOR FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: US 60/284,555

; PRIOR FILING DATE: 2001-04-17

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 39

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

FEATURE:

; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member

; OTHER INFORMATION: 17 (TNFRSF17)

US-10-087-080-39

Query Match 100.0%; Score 964; DB 15; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.9e-90;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCL 60

Db 1 MLQWAGCQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKS 180

Db 121 YTEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184

Db 181 ISAR 184

RESULT 12

US-09-854-864-5

; Sequence 5, Application US/09854864

; Publication No. US20020081296A1

GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; TITLE OF INVENTION: BLYS/AGF-3, AND TACI

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-5

Query Match

Best Local Similarity 98.5%; Score 950; DB 9; Length 181;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCLGLS 63

Db 1 MAGQCSQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCLGLS 60

Qy 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 123

Db 61 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 120

Qy 124 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSISA 183

Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSISA 180

Qy 184 R 184

Db 181 R 181

RESULT 13

US-09-855-158-5

; Sequence 5, Application US/09855158

; Publication No. US20020086018A1

GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, B

; TITLE OF INVENTION: 3, AND TACI

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-5

Query Match

Best Local Similarity 98.5%; Score 950; DB 9; Length 181;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCLGLS 63

Db 1 MAGQCSQNEFYDLSLHACIPQLRCSSNTPLTCORYCNASVTSVKGTTNAILWTCLGLS 60

Qy 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 123

Db 61 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLETV 120

Qy 124 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSISA 183

Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCKSLPAALSATEIEKSISA 180

Qy 184 R 184

Db 181 R 181

RESULT 14

US-09-854-864-11

; Sequence 11, Application US/09854864

; Patent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 185
TYPE: PRT
ORGANISM: Murine
US-09-854-864-11

Query Match 59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 2.6e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
QY 4 MAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
DB 1 MAQCCFHSYFDSLLHACKFCHLRCSN--PPATCQPCDPSVTSSVKGTYYVLWIFLGLT 58
QY 64 LIISLAVFVLMFLRLKISSEPLKDEPKN----TGSGLLGMANIDLEKSTGTDEIILPRGL 119
DB 59 LVLSLALFTISFLLRKNPEALKDEPQSPQLDGSQAQLDKADTELTRIRAGDDRIFPRSL 118
QY 120 EYTVRECTCEDCKSPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
DB 119 EYTVRECTCEDCKSPKRGSDHFFPLPAMEGATILVTTKTNDYCKSSVPTALQSVNGM 178
QY 178 EKSISAR 184
DB 179 EKPTHTR 185

RESULT 15
US-09-855-158-11
Sequence 11, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 185
TYPE: PRT
ORGANISM: Murine
US-09-855-158-11

Query Match 59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 2.6e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
QY 4 MAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
DB 1 MAQCCFHSYFDSLLHACKFCHLRCSN--PPATCQPCDPSVTSSVKGTYYVLWIFLGLT 58
QY 64 LIISLAVFVLMFLRLKISSEPLKDEPKN----TGSGLLGMANIDLEKSTGTDEIILPRGL 119

DB 59 LVLSLALFTISFLLRKNPEALKDEPQSPQLDGSQAQLDKADTELTRIRAGDDRIFPRSL 118
QY 120 EYTVRECTCEDCKSPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
DB 119 EYTVRECTCEDCKSPKRGSDHFFPLPAMEGATILVTTKTNDYCKSSVPTALQSVNGM 178
QY 178 EKSISAR 184
DB 179 EKPTHTR 185

Search completed: February 26, 2005, 21:04:28
Job time : 140.37 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	964	100.0	184	2	S43486	B-cell maturation
2	88.5	9.2	217	2	C97344	amino acid ABC tra
3	86.5	9.0	858	2	T08881	prominin - mouse
4	83.5	8.7	1998	2	T13009	hypothetical prote
5	82	8.5	1009	2	A57434	protein-tyrosine k
6	81.5	8.5	2233	2	T28669	surface protein 51
7	81	8.4	773	2	D89010	protein R08F11.7
8	79.5	8.2	1009	2	S60248	protein-tyrosine k
9	79.5	8.2	1299	2	T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2	D64469	potassium channel
11	78	8.1	841	2	JCS5894	killer cell inhibi
12	77.5	8.0	738	2	D86345	hypothetical prote
13	77.5	8.0	968	2	T01733	hypothetical prote
14	77	8.0	522	2	T45824	hypothetical prote
15	77	8.0	539	2	F72288	methyl-accepting c
16	76.5	7.9	357	2	T21152	hypothetical prote
17	76.5	7.9	1404	2	T19277	hypothetical prote
18	76	7.9	744	2	A43353	ascites siialoglyco
19	76	7.9	748	2	T47250	complex I intermed
20	75.5	7.8	638	2	T41478	probable transcript
21	75	7.8	450	2	B97297	hydrogenase chain
22	75	7.8	857	1	A41369	S-receptor kinase
23	74.5	7.7	384	2	S45592	ERD1 protein - yea
24	74.5	7.7	1101	2	T16840	hypothetical prote
25	74	7.7	377	2	JC7535	chitinase (EC 3.2.
26	73.5	7.6	307	2	B95039	membrane protein
27	73.5	7.6	307	2	A97967	conserved hypothet
28	73	7.6	304	2	A89882	hypothetical prote
29	73	7.6	679	2	B96599	protein F20N2.12

QY	78	KRISSEPLKDEFKNTGSGLLGMANIDLEKSRGD-EIIL---	PRGLEVTVVEECTCE---	129
DB	168	GFVANOQTRIKGTQK-----	LAKSNFRDFQTLLETPTFKQIDYVVEQYNTNKKA	218
QY	130	-----DCIKS-----	KPKVDSHCHCFPLPAMEEGATILVTK-TNDYCKSLPAL--	172
DB	219	FSDLDIGSGVLGRIKDQLPKV-----	TPVLEIKAMATAIKQTKDALQNMSSSLKS	271
QY	173	-----SATEIEKSISA	183	
DB	272	LQDAATQLNTNLSS	285	
RESULT 4				
T13009				
hypoetical protein T24C20.80 - Arabidopsis thaliana				
C:Species: Arabidopsis thaliana (mouse-ear cress)				
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004				
C:Accession: T13009				
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenav				
submitted to the Protein Sequence Database, July 1999				
A:Reference number: Z17586				
A:Accession: T13009				
A:Molecule type: DNA				
A:Residues: 1-1998 <CHO>				
A:Cross-references: UNIPROT:Q8STR8; EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.8				
A:Experimental source: cultivar Columbia; BAC clone T24C20				
C:Genetics:				
A:Gene: ATSP:T24C20.80				
A:Map position: 3				
A:Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1;				
C:Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80				
Query Match 8.7%; Score 83.5; DB 2; Length 1998;				
Best Local Similarity 29.4%; Pred. No. 26;				
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;				
QY	38	ORYCNASVNSVKGTNAILWTCLGLSLIISLAVFLMFLRLKRISSEPLKD-EFKN--TGS	94	
DB	1089	ERYCSA---NSALGTFSM---C-----	SSTGPFQDSEFENFSLGP	1122
QY	95	GLLGMANIDLEKSRGDEILPRLGLYTVVEECTCEPICSKP-----	KVDSHCFPLPAM	149
DB	1123	SLVKLSSLDN--SRIGD-----	RGIHFDEGGSCNGRSSAPGLTGNVNDMCGDL--M	173
QY	150	EGGATI 155		
DB	1174	DGGATI 1179		
RESULT 5				
A57434				
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat				
N;Alternate names: cell adhesion kinase-beta				
C:Species: Rattus norvegicus (Norway rat)				
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004				
C:Accession: A57434				
R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.				
J. Biol. Chem. 270, 21206-21219, 1995				
A:Title: Cloning and characterization of cell adhesion kinase beta, a novel pro				
A:Reference number: A57434; MUID:95403356; PMID:7673154				
A:Accession: A57434				
A>Status: preliminary				
A:Molecule type: mRNA				
A:Residues: 1-1009 <SAS>				
A:Cross-references: UNIPROT:P70600; GB:D45854; NID:g1000679; PIDN:BA08290.1; F				
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kina				
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase				
F;423-686/Domain: protein kinase homology <KIN>				
F;431-439/Region: protein kinase ATP-binding motif				
Query Match 8.5%; Score 82; DB 2; Length 1009;				

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C/Species: Spodoptera frugiperda (fall armyworm)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43251
R/Cleplik, M.; Klenk, H.
A/Submitted to the EMBL Data Library, January 1996
A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A/Reference number: 223368
A/Accession: T43251
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1299 <CIE>
A/Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:gl167859; PID:e219690; PIDN:CAA9311
A/Experimental source: clone Sfurin 6; ovary
C/Function:
A/Description: responsible for the endoproteolytic processing of proproteins with specific
C/Keywords: hydrolase; serine proteinase

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
Best Local Similarity 24.1%; Pred. No. 40;
Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFDLSLHACIPCOLRCS-----SNTPLTCORYCNAS-----VTNSVKGTHAIL-W 57
Db 1150 CSRPLRIDRLNNQVPC---CSERGVTNSTPTDC-CHCNPENGECINSVAGKRRIAEW 1205
QY 58 TGLGLS-----LIISLAV-----FVLMFLRLKISSEPLKDEFKNTGSLGGMAN 101
Db 1206 GALHTAPSADAPSVAVVTIAVCAAAVGLFITVVLVLAHSREKTRKTSVRG----- 1259
QY 102 IDLEKSRGTDEILPR-GLETVVECTCSDCKSKPKVDSH 142
Db 1260 --VEYSR-----LPTDVFDTV-----LTSCTDQEGFVEYEH 1289

RESULT 10
D64469
potassium channel homolog - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: D64469
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: D64469
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-343 <BUL>
A/Cross-references: UNIPROT:Q58752; GB:U67575; GB:L77117; NID:gl591992; PIDN:AAB99365.1;
C/Genetics:
A/Map position: REV1308326-1307295
C/Superfamily: conserved hypothetical protein sl10993

Query Match 8.1%; Score 78.5; DB 2; Length 343;
Best Local Similarity 20.4%; Pred. No. 13;
Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

QY 12 EYFDLSLHACIPCOLRCSNTPLTCORYCNASVTNSVKGTHAILWTCGLSLIISLAVF 71
Db 32 DYFALYFSVI-----TITTYGDFTPKTFGLRGLTVVYLCVGVGVIMYFSL 80
QY 72 VLMFL-----LRKISS--EPLKDFKNTGSLGMA-----NIDLEKSRGTGD 111
Db 81 IAEFIVEGFEFVRLKMKNKIKLKHVYICGYGLGVKGVCEKFEENIPPIADINE 140
QY 112 EII-----LPRGLETVVECTCSDCKSKPKV-----DSDHCF-PLPAMEEG 152
Db 141 DVLKEEYKYPDKFLYIVGDARKEEVILK-KAKIDKAKGLIATLPSPADNVFLTLTARELN 199

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C/Species: Spodoptera frugiperda (fall armyworm)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43251
R/Cleplik, M.; Klenk, H.
A/Submitted to the EMBL Data Library, January 1996
A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A/Reference number: 223368
A/Accession: T43251
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1299 <CIE>
A/Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:gl167859; PID:e219690; PIDN:CAA9311
A/Experimental source: clone Sfurin 6; ovary
C/Function:
A/Description: responsible for the endoproteolytic processing of proproteins with specific
C/Keywords: hydrolase; serine proteinase

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
Best Local Similarity 24.1%; Pred. No. 40;
Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFDLSLHACIPCOLRCS-----SNTPLTCORYCNAS-----VTNSVKGTHAIL-W 57
Db 1150 CSRPLRIDRLNNQVPC---CSERGVTNSTPTDC-CHCNPENGECINSVAGKRRIAEW 1205
QY 58 TGLGLS-----LIISLAV-----FVLMFLRLKISSEPLKDEFKNTGSLGGMAN 101
Db 1206 GALHTAPSADAPSVAVVTIAVCAAAVGLFITVVLVLAHSREKTRKTSVRG----- 1259
QY 102 IDLEKSRGTDEILPR-GLETVVECTCSDCKSKPKVDSH 142
Db 1260 --VEYSR-----LPTDVFDTV-----LTSCTDQEGFVEYEH 1289

RESULT 10
D64469
potassium channel homolog - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: D64469
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: D64469
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-343 <BUL>
A/Cross-references: UNIPROT:Q58752; GB:U67575; GB:L77117; NID:gl591992; PIDN:AAB99365.1;
C/Genetics:
A/Map position: REV1308326-1307295
C/Superfamily: conserved hypothetical protein sl10993

Query Match 8.1%; Score 78.5; DB 2; Length 343;
Best Local Similarity 20.4%; Pred. No. 13;
Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

QY 12 EYFDLSLHACIPCOLRCSNTPLTCORYCNASVTNSVKGTHAILWTCGLSLIISLAVF 71
Db 32 DYFALYFSVI-----TITTYGDFTPKTFGLRGLTVVYLCVGVGVIMYFSL 80
QY 72 VLMFL-----LRKISS--EPLKDFKNTGSLGMA-----NIDLEKSRGTGD 111
Db 81 IAEFIVEGFEFVRLKMKNKIKLKHVYICGYGLGVKGVCEKFEENIPPIADINE 140
QY 112 EII-----LPRGLETVVECTCSDCKSKPKV-----DSDHCF-PLPAMEEG 152
Db 141 DVLKEEYKYPDKFLYIVGDARKEEVILK-KAKIDKAKGLIATLPSPADNVFLTLTARELN 199

QY 153 ATILVTTKND 163
Db 200 PHILITAKADE 210

RESULT 11
JC5894
killer cell inhibitory receptor p91A precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
C/Accession: JC5894
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohy;
J. Biochem. 123, 358-368, 1998
A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A/Reference number: JC5894; MUID:98218758; PMID:9538215
A/Accession: JC5894
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-841 <YAM>
A/Cross-references: UNIPROT:Q8R2Z1; GB:AF040946
A/Comment: This protein function as inhibitory cell-surface molecule against cell activ
C/Genetics:
A/Map position: 7
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
F/24-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #status I
F/636-674/Domain: transmembrane #status predicted <TM>
F/675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 8.1%; Score 78; DB 2; Length 841;
Best Local Similarity 22.7%; Pred. No. 35;
Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

QY 9 SQNEYFDLSLHACIPCOLRCS-----SNTPLTCORYCNASVTNSVKGTHAILWTCGLSL 64
Db 598 AQNSSFYLLSSASAPVELTVSGPIETSTPTPT-----MSMPLGGLHMYLKALIGSV 649
QY 65 IISLAVFVLMFL--RKISSBPKDEFKNTGSLGGMANIDLEKSRGTDEILPRG---- 118
Db 650 AFILFELIFILFILLRRHGRKRDVQEK-----DLQLSSGAEEPTIRKGLQK 699
QY 119 -----LEVTVBECTCEDCIK-----SKPKVSDHCFPLPAMEGATILVTTKN 162
Db 700 RNPAAATQESLYASVEDMQTDGVELNSWTTPED-----PQGET----- 741
QY 163 DYCKSLPAAL-SATEIEKSISAR 184
Db 742 -YQVKPSRLRKAGHVSPVMSR 763

RESULT 12
D86345
hypothetical protein Fl6F4.10 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D86345
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: D86345
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-738 <STO>
A/Cross-references: UNIPROT:Q9LMN6; GB:AE005172; NID:g8920639; PIDN:AAF81361.1; GSPDB:G
C/Genetics:

```

A:Map position: 1
C:Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; pro
Query Match 8.0%; Score 77.5; DB 2; Length 738;
Best Local Similarity 26.2%; Pred. No. 34;
Matches 28; Conservative 21; Mismatches 45; Indels 13; Gaps 5;

Qy 8 CSQNEYFDSLL-HACIFCOLRCSNTPLTCQRYCNASVTNSVKGVTNAILWTCLGLSLII 66
Db 294 CSGDSTCENKLGHFRCRCRYSYELNTTNTCKPGNPEY---VEWTTIVLGTIGF-LVI 349
Qy 67 SLAVFVLMLFLLRKISSBPLKDE-FKNTGSGLL-----GMANIDLE 105
Db 350 LLAISCTEHKWKNTYDTELRQQFQEGGGMQLMORLSGAGPSNVDRVK 396

RESULT 13
T01733
hypothetical protein A IG002N01.31 - Arabidopsis thaliana
C:Species: Arabidopsis_thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01733
R:Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002N01.
A:Reference number: Z14407
A:Accession: T01733
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-968 <SCH>
A:Cross-references: UNIPROT:O04623; EMBL:AF007269; NID:g2191126; PID:g2191152
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;
A:Note: A IG002N01.31

```

```

Query Match      8.0%; Score 77.5; DB 2; Length 968;
Best Local Similarity 21.6%; Pred. No. 45;
Matches 35; Conservative 26; Mismatches 62; Indels 39; Gaps 5;

QY..    43 ASVTNSVKG---TNAIWTCLGLSLIIISIAVFVLM-----FLLRKISSSEPLK 86
       :|::||: ||: ||::||: ||: ||: ||: ||: |
Db   770 SLDLDSIGVGESSDGVSGVALGVAAGLSVSFAFTEDRKQTLLKVDFLNTKVPARELV 829
       :|::||: ||: ||::||: ||: ||: ||: ||: |
QY     87 DEFKNRTGSGLGMANIDLEKSRTGDEILPRGLEYYVEECTCEDCIKSKEPKVSDHCFPL 146
       :|::||: ||: ||::||: ||: ||: ||: ||: |
Db   830 DELKEIKCAL-----LPQSTSNKALPAPATVTAESAATATTITTVDKP----- 872
       :|::||: ||: ||::||: ||: ||: ||: ||: |
QY    147 PAMEEGATILTITKYND----YCKSLPAALSATEIEKSISAR 184
       :|::||: ||: ||::||: ||: ||: ||: ||: |
Db   873 --VPEPETAAATTTVDKPVEPEPEPVPPVPAIEAATAAQ 912
       :|::||: ||: ||::||: ||: ||: ||: ||: |

RESULT 14
T45824
hypothetical protein F2KI5.50 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45824
R/Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A/Reference number: 223015
A/Accession: T45824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-522 <RIE>
A/Cross-references: UNIPROT-Q9M3B3; EMBL.ALJ32956
A/Experimental source: cultivar Columbia; BAC clone F2KL5
C/Genetics:
A/Map position: 3
A/Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3
A/Note: F2KI5.50
```

C:Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70

Query Match 8.0%; Score 77; DB 2; Length 522;
Best Local Similarity 27.0%; Pred. No. 27;
Matches 27; Conservative 18; Mismatches 37; Indels 18; Gaps 3

Qy 16 SLLHAC-----IPQLRCSSNTPLTCQRYCNASVTSVKGNTNAILWTC--IG 61
Db 159 SLVLACMRKTSNPDELPSLPQYQYSSRSLSLTGTGRSDSRLLMLVK---VIMTAVILG 214
Qy 62 LSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMAN 101
Db 215 LNTVCDALFIVTTLFVKQDETPIKGDPLSTKSKQLRLVH 254

RESULT 15
F72288 methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: F72288
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.J.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-539 <ARN>
A:Cross-references: UNIPROT:Q9XON0; GB:AE001772; GB:AE000512; NID:g4981693; PIR:Q9XON0
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1146
C:Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
Best Local Similarity 32.0%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5

Qy 42 NASVTSVKGNTNAILWTCIGLSLIISLAVFVLMFLRLKISSEPLKD---EFKNTGSGLLG 98
Db 150 NVSMTRNIK-RNIFF----LVVCAAMFIAITFTRLTT-PLKKLAVLENLSHGVL- 202
Qy 99 MANIDLEKSRGTDEI 113
Db 203 --NVEIEKIRSKDEI 215

Search completed: February 26, 2005, 21:05:24
Job time : 41.366 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:37:33 ; Search time 176.953 Seconds
(without alignments)
532.472 Million cell updates/sec

Title: US-10-077-438-1
Perfect score: 964
Sequence: 1 MLQMGQCQSQNEYFDSLHA.....CKSLPALGATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	1 TR17_HUMAN	Q02223 homo sapien
2	960	99.6	184	2 O6PE46	O6PE46 homo sapien
3	572	59.3	185	1 TR17_MOUSE	O88472 mus musculus
4	116.5	12.1	175	1 T13C_MOUSE	O9d8d0 mus musculus
5	116.5	12.1	175	2 O8R4W8	O8R4W8 mus musculus
6	94	9.8	323	1 TNRC_BOVIN	P51867 bos taurus
7	93	9.6	184	1 T13C_HUMAN	O96tj3 homo sapien
8	92.5	9.6	334	2 O6VT98	O6vt98 symbiont ba
9	89	9.2	3005	2 O6BFG4	O6bf94 paramecium
10	88.5	9.2	217	2 O97D61	O97d61 clostridium
11	86.5	9.0	804	2 O80XB2	O80xb3 mus musculus
12	86.5	9.0	809	2 O80XB2	O80xb2 mus musculus
13	86.5	9.0	823	2 O80XB6	O80xb6 mus musculus
14	86.5	9.0	827	2 O8CDK8	O8cdk8 mus musculus
15	86.5	9.0	834	2 O8BH12	O8bh12 mus musculus
16	86.5	9.0	842	2 O8R056	O8r056 mus musculus
17	86.5	9.0	867	1 PML1_MOUSE	O54990 mus musculus
18	86	8.9	1309	2 O6CCL1	O6ccl1 yarrowia li
19	85.5	8.9	1193	2 O9Y1X8	O9y1x8 ephydatia f
20	83.5	8.7	938	2 O8RWV7	O8rwv7 arabidopsis
21	83.5	8.7	1998	2 O9STR8	O9str8 arabidopsis
22	83	8.6	449	2 O8C6R5	O8c6r5 mus musculus
23	83	8.6	474	2 O8C9L4	O8c9l4 mus musculus
24	82.5	8.6	164	2 O7RAA5	O7raa5 plasmodium
25	82.5	8.6	1142	2 O6CCL7	O6ccl7 yarrowia li
26	82	8.5	327	2 O97491	O97491 oviss aries
27	82	8.5	967	2 O8C2G0	O8c2g0 mus musculus
28	82	8.5	1009	1 FAK2_MOUSE	O9qvd9 m protein t
29	82	8.5	1009	1 FAK2_RAT	P70600 rattus norv
30	81.5	8.5	314	2 O8VSV6	O8vev6 mus musculus
31	81.5	8.5	2233	2 O94711	O94711 paramecium

RESULT 1

ID	TR17_HUMAN	STANDARD;	PRT;	184 AA.
AC	Q02223;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).			
DE	maturatation protein).			
GN	Name=TNFRSF17; Synonyms=BCM, BCMA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.			
RP	TISSUE=Lymph node, and Peripheral blood leukocytes;			
RC	MEDLINE=93010984; PubMed=1396583;			
RA	Laabi Y., Gras M.F., Carbonnel F., Brouet J.C., Berger R.,			
RA	Larsen C.J., Tsapis A.;			
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;pl3) translocation in a malignant T cell lymphoma."			
RL	EMBO J. 11:3897-3904(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=94218235; PubMed=8165126;			
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed."			
RL	Nucleic Acids Res. 22:1147-1154(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;			
RA	Lofthus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,			
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,			
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,			
RA	Richler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q."			
RL	Genomics 60:295-308(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.			
RP	MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;			
RA	Kawasaki A., Teuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;			
RT	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis."			
RL	Genes Immun. 2:276-279(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; ASN-81 AND SER-165.			
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,			
RA	Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,			
RA	Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;			

Q39191 arabidopsis
O01892 caenorhabdi
Q7TQ99 mus musculu
O8IN39 drosophila
O81820 arabidopsis
Q8kiyi pseudomonas
Q14289 h protein t
O6pid4 homo sapien
Q26489 spodoptera
O65T73 mantheinia
Q7R6V0 plasmodium
Q80281 fugu rubrip
O14836 homo sapien
Q8VFW0 mus musculu

"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>)."; Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

[6]

RP FUNCTION: AND INTERACTIONS WITH TRAF1 AND TRAF3.

RX MEDLINE=20363816; PubMed=10903733;

RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J.-I., Devergne O., Teaple A.;

RA "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-activated protein kinase.";

RT J. Immunol. 165:1322-1330 (2000).

[7]

RP FUNCTION.

RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;

RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.;

RA "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell autoimmune disease.";

RT Nature 404:995-999 (2000).

[8]

RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.

RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;

RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;

RA "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating humoral immunity.";

RT Nat. Immunol. 1:252-256 (2000).

[9]

RP INTERACTIONS WITH TRAF5 AND TRAF6.

RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;

RA Shu H.-B., Johnson H.;

RA "B cell maturation protein is a receptor for the tumor necrosis factor family member TALL-1.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161 (2000).

CC -!- FUNCTION: Receptor for TNFSF13B/Blys/BAFF and TNFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK.

CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.

CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.

CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-cells or monocytes.

CC -!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia (T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which involves TNFSF17 and IL2.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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CC EMBL; Z14954; CAA78679.1; -

CC EMBL; Z29575; CAA82691.1; -

CC EMBL; Z29574; CAA82690.1; -

CC EMBL; U95742; AAB67251.1; -

CC EMBL; AB052772; BAB60895.1; -

CC EMBL; AY509112; AAR84240.1; -

CC PIR; S43486; S43486.

CC PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.

CC Genew; HGNC:11913; TNFSF17.

CC MIM; 109545; -

CC GO; GO:0016021; C:integral to membrane; TAS.

CC GO; GO:0005886; C:plasma membrane; TAS.

CC GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0008283; P:cell proliferation; TAS.

DR GO; GO:0007275; P:development; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

KW 3D-structure; Chromosomal translocation; Immune response;

KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.

FT DOMAIN 1 54 Extracellular (Potential).

FT TRANSMEM 55 77 Signal-anchor for type III membrane protein (Potential).

FT DOMAIN 78 184 Cytoplasmic (Potential).

FT REPEAT 7 41 TNFR-Cys.

FT SITE 3 4 Breakpoint for translocation to form IL2/TNFRSF17 oncogene.

FT DISULFID 8 21 By similarity.

FT DISULFID 24 37 By similarity.

FT DISULFID 28 41 By similarity.

FT VARIANT 54 54 A -> V.

FT VARIANT 65 65 /FTID=VAR_018755.

FT VARIANT 75 75 /FTID=VAR_018756.

FT VARIANT 81 81 /FTID=VAR_018757.

FT VARIANT 153 153 /FTID=VAR_018758.

FT VARIANT 165 165 /FTID=VAR_012234.

FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.8e-81;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWAGQSQNEYFDSLHACIPQLCRSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60

Db 1 MLWAGQSQNEYFDSLHACIPQLCRSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60

QY 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGEIILPRGLE 120

Db 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTGEIILPRGLE 120

QY 121 YVVECTCEDCICKPKVDSHCPFLPAMEGATILVTTKNDYCKSLPAALSATEIKS 180

Db 121 YVVECTCEDCICKPKVDSHCPFLPAMEGATILVTTKNDYCKSLPAALSATEIKS 180

QY 181 ISAR 184

Db 181 ISAR 184

RESULT 2

Q6PE46 PRELIMINARY; PRT; 184 AA.

ID Q6PE46; AC Q6PE46; DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Tumor necrosis factor receptor superfamily, member 17.

GN Name=TNFRSF17;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

RP [1]_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Pooled;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Mordan J.P., Berger R., Tsapis A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski A.C., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RC Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAF58291.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

 Query Match 99.6%; Score 960; DB 2; Length 184;
 Best Local Similarity 99.5%; Pred. No. 4.2e-81;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MUQAGCCSQNEFYDSLLHACIPQLRCSNTPLTCORYCNASVTSVNGTNAIWTCL 60
 DB 1 MUQAGCCSQNEFYDSLLHACIPQLRCSNTPLTCORYCNASVTSVNGTNAIWTCL 60

 QY 61 GUSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANTIDLEKSRGTDEILPRGLE 120
 DB 61 GUSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANTIDLEKSRGTDEILPRGLE 120

 QY 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

 QY 181 ISAR 184
 DB 181 ISAR 184

 RESULT 3
 TR17_MOUSE STANDARD; PRT; 185 AA.
 AC O88472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN Name=Tnfrsf17; Synonyms=BCM, BCMA;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
 RA "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.C., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL CC
 CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O88472-2; Sequence=VSP_006507;
 CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC
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CC EMBL; AF061505; AAC23799.1; --
CC EMBL; AK020247; BAB32038.1; --
CC EMBL; BC027519; AAH27519.1; --
CC HSSP; Q02223; 100D.
DR MGD; MGI:1343050; Tnfrsf17.
DR Alternative splicing; Immune response; Receptor; Signal-anchor;
KW Transmembrane. 1 49 Extracellular (Potential).
FT DOMAIN 50 70 Signal-anchor for type III membrane
FT TRANSMEM 50 70 protein (Potential).
FT DOMAIN 71 185 Cytoplasmic (Potential).
FT REPEAT 4 36 TNFR-Cys.
FT DISULFID 5 18 By similarity.
FT DISULFID 21 32 By similarity.
FT DISULFID 25 36 By similarity.
FT VARSPLIC 87 91 Missing (in isoform 2).
FT /FTID=VSP 006507.
FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;
Query Match 59.3%; Score 572; DB 1; Length 185;
Best Local Similarity 62.8%; Pred. No. 4.7e-45;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
QY 4 MAGQCSONEYFDSLLHACIPQCLRCSSNTPPLTCQRYCNASVTSYKGNALWTCGLGS 63
DB 1 MAQCQHFSEYFDSLLHACKEHLRCNS--PPATCQPCDPSTSSVKGTYVTLWIFLGLT 58
QY 64 LIISLAVFVLMFLRKISSEPLKDFKN-----TGSLLGNANIDLEKSTGDEIILPRL 119
DB 59 LVLSLALFTISFLLRKNMPEALDEPQSQQLDGSAGLQKADTELTRIRAGDDRIIPREL 118
QY 120 EYTVETCTCEDCTKSKPKVSDHCFPLPAMEGATILVTTKNDYCK-SLPAAL-SATRI 177
DB 119 EYTVETCTCEDCVKSKPKGSDHFFPLPAMEGATILVTTKGDKSSVPTALQSVGM 178
QY 178 EKISAR 184
DB 179 EKPTHTR 185
RESULT 4
T13C MOUSE : STANDARD; PRT; 175 AA.
AC Q98D0; ID T13C MOUSE : STANDARD; PRT; 175 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3)
DE (B-cell maturation defect).
GN Name=Tnfrsf13c; Synonyms=Baffr, Bcmd, Br3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALE/c; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Teschopp J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF";
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;
RX MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;

RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency.";
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takerana Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Sasaki D., Waterston R., Landier E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;
RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
RA Hilbert D.M., Hayes C.E., Cancro M.P.;
RT "Competition for Blys-mediated signaling through Bcmd/BR3 regulates
RT peripheral B lymphocyte numbers.";
RL Curr. Biol. 11:1986-1989(2001).
CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/Blys.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q98D0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q98D0-2; Sequence=VSP 006506;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC detected at lower levels in lung and thymus.
CC -!- DISEASE: Defects in Tnfrsf13c are a cause of severe B-cell
CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
CC is not detectable. B-cell lymphopoiesis is normal, but the life
CC span of peripheral B-cells is much reduced.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
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```
DR EMBL; AK008142; BAB25490.1; -.
DR HSP; Q96R33; 10QE.
DR MGD; MGI:1919299; Tnfrsf33c.
KW Alternative splicing; Glycoprotein; Immune response; Receptor;
KW Signal-anchor; Transmembrane.
FT DOMAIN 72 92 Extracellular (Potential).
FT TRANSMEM 72 92 Signal-anchor for type III membrane
protein (Potential).
FT DOMAIN 93 175 Cytoplasmic (Potential).
FT REPEAT 21 38 TNFR-Cys (incomplete).
FT FT DISULFID 22 35 By similarity.
FT FT CARBOHYD 27 38 By similarity.
FT FT VARSPLIC 133 143 N-linked (GlcNAc...) (Potential).
FT FT Missing (in isoform 2).
FT FT /Fid:VSP_006506.
SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 12.1%; Score 116.5; DB 1; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.0091;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSQNEYFDSLLHACIPCOL-----RCSSTNPPLTCQRYCNASVTNSVK---GTNAIL 56
Db 21 QCNQTECFDPLVNCVSCELFHTPDGHTSSLEFGTALQPEGALRDPVALLVGAPALL 80
QY 57 WTCIGLSLI--ISLAVFLMFLRKIS---SEPLKDFKNTGSLGGMANIDLEKSRGTGD 111
Db 81 GLIALTLVGLSVLRWNRQLRTASPDTSQVQOE-----SLENVFPVSSET-- 129
QY 112 EIIPLRGLEVTVECTCDICKPKVDSDHCFPLPAMEGATILYTTKT 161
Db 130 ----PHASAPTWPPLK-EDADSALPR-----HSVFPVPATELGSTELVTTKT 170

RESULT 5
Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002 (T:EMBLrel. 21, Created)
DT 01-JUN-2002 (T:EMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (T:EMBLrel. 24, Last annotation update)
DE TRAF3 binding protein.
GN Name=Tnfrsf33c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL83914.1; -.
DR HSP; Q96R33; 10QE.
DR MGD; MGI:1919299; Tnfrsf33c.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 175 AA; 18846 MW; B64BFF4B52BE93B1 CRC64;

Query Match 12.1%; Score 116.5; DB 2; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.0091;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSQNEYFDSLLHACIPCOL-----RCSSTNPPLTCQRYCNASVTNSVK---GTNAIL 56
Db 21 QCNQTECFDPLVNCVSCELFHTPDGHTSSLEFGTALQPEGALRDPVALLVGAPALL 80
QY 57 WTCIGLSLI--ISLAVFLMFLRKIS---SEPLKDFKNTGSLGGMANIDLEKSRGTGD 111
Db 81 GLIALTLVGLSVLRWNRQLRTASPDTSQVQOE-----SLENVFPVSSET-- 129
QY 112 EIIPLRGLEVTVECTCDICKPKVDSDHCFPLPAMEGATILYTTKT 161
Db 130 ----PHASAPTWPPLK-EDADSALPR-----HSVFPVPATELGSTELVTTKT 170
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RESULT 6
TNR6_BOVIN STANDARD; PRT; 323 AA.
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51857;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95 antigen).
GN Name=TNR6; Synonyms=APT1, FAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoo J., Stone R.T., Beattie C.W.;
RT Cloning and characterization of the bovine Fas.;
RL DNA Cell Biol. 15:227-234(1996).
CC -!- FUNCTION: Receptor for TNFRsf6/FASL. The adaptor molecule FADD
recruits caspase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteolytic
activation which initiates the subsequent cascade of caspases
(aspartate-specific cysteine proteases) mediating apoptosis. FAS-
mediated apoptosis may have a role in the induction of peripheral
tolerance, in the antigen-stimulated suicide of mature T-cells, or
both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Contains a death domain involved in the binding of FADD,
and maybe to other cytosolic adaptor proteins.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
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DR EMBL; U34794; AAC48546.1; -.
DR HSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death_1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 323 Tumor necrosis factor receptor
superfamily member 6.
FT DOMAIN 17 170 Extracellular (Potential).
FT TRANSMEM 171 198 Potential.
FT DOMAIN 189 323 Cytoplasmic (Potential).
FT REPEAT 45 80 TNFR-Cys 1.
FT REPEAT 81 124 TNFR-Cys 2.
FT REPEAT 125 163 TNFR-Cys 3.
FT DOMAIN 238 306 Death.
FT DISULFID 45 56 By similarity.
FT DISULFID 57 70 By similarity.
```

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CC Name=2;
CC IsoId=Q96RJ3-2; Sequence=VSP_006505;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC in resting B-cells. Detected at lower levels in activated B-cells,
CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
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CC -----
CC EMBL; AF373846; AAK91826.1; -.
CC PDB; 1MPV; NMR; A=23-35.
CC PDB; 1OOE; X-ray; K/L/M/N/O/P/Q/R=16-46.
CC PDB; 1OSK; NMR; A=1-61.
CC Genew; HGNC:17755; TNFRSF13C.
CC MIM; 608269; -.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
CC PROSITE; PSS0050; TNFR_NGFR_2; FALSE NEG.
CC 3D-structure; Alternative splicing; Immune response; Receptor;
CC Signal-anchor; Transmembrane.
CC DOMAIN 1 78 Extracellular (Potential).
CC TRANSMEM 79 99 Signal-anchor for type III membrane
CC protein (Potential).
CC FT DOMAIN 100 184 Cytoplasmic (Potential).
CC REPEAT 18 35 TNFR-Cys (incomplete).
CC FT DISULFID 19 32 By similarity.
CC FT DISULFID 24 35 By similarity.
CC FT VARSPLIC 143 143 P -> PA (in isoform 2).
CC FT SEQUENCE 184 AA; 18863 MW; F2BFB98099A27138 CRC64;
CC /FTID=VSP_006505.
CC -----
Query Match 9.6%; Score 93; DB 1; Length 184;
Best Local Similarity 26.5%; Pred. No. 1.5;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEVFDSLHACIPCOL-----RCSSNTP--PLTCQRYCNASVTVNSVKGTTNAIL 56
DB 19 CVPAECFDLLVRHCVACGLLTPRPDPAGASSPAPRTALQPQESVGVAGAGEAALPLFCLL 78
QY 57 W---TCIGLSLIISLAVFLVMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
DB 79 FGAPALLGLALVLALVLGLVSVRRORRLRGASSAEAPGDKDAPEPL----- 127
QY 108 RTGDEIILPRLGLEYTVVECTC-----EDCIKSKPVDSDDHCFPLPAMEGATILVTK 160
DB 128 ---DKVII---LSFGISDATAPAWPPGPDGTTTP---CHSVFVPATELGLSTELVTK 177
QY 161 T 161
DB 178 T 178
-----
RESULT 8
Q6VT98 PRELIMINARY; PRT; 334 AA.
ID Q6VT98;
AC Q6VT98;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative acyltransferase.
GN Name=pedC;
OS symbiont bacterium of Paederus fuscipes.
OC Bacteria.
OX NCBI_TaxID=176282;
RN [1]
RP SEQUENCE FROM N.A.

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DR InterPro: IPR009030; Grow_fac_recept.
DR SMART: IPR006210; IEGF.
DR SMART: SM00181; EGF; 22.
DR SMART: SM00261; FU; 29.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; UNKNOWN_1.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; 12.
SQ SEQUENCE 3005 AA; 343921 MW; D8CC6A247876A5A5 CRC64;

Query Match 9.2%; Score 89; DB 2; Length 3005;
Best Local Similarity 20.3%; Pred. No. 63;
Matches 48; Conservative 26; Mismatches 59; Indels 104; Gaps 13;

QY 1 MLOMAQCQ-SONEYFDSLHACIPCOLRGSSNTPPLTQC-----RYC----- 41
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 1177 ILKVGNGQCLCKDGYFESSTNQICTQDLSC-----FTCGSSKCYCLCDPAFHLQSLNQN 1230
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 42 -----NASVNSVKGTVNAILWTCLGLSLIISLAVFLMLRLKISSSEPL-----K 86
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 1231 KCICDSGYFNTS-TKQCACNMTCKECSVS-----QCIECEPMTTYNDR 1275
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 87 DEFPKNTGSGLLGMANIDLEKSRGTDEIILPRGLEIYVE-----ECTCEDCIKSKPKV-- 138
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 1276 DTFK-----CLCKDGYETIEIKWCQPCDMTCKTCVSQSTKCLT 1313
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 139 -----DSDHCPLPAMBE-GATILVTTKNDYCKSLPA-----ALSTETBEK 179
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 1314 CBSIHLRSPFNSNKC---PCLDGYFDVGIEMQCKNDLCKTQCSISTQCLSCVETE 1367
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

RESULT 10
Q97D61 PRELIMINARY; PRT; 217 AA.
ID Q97D61 AC Q97D61
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amino acid ABC transporter, permease component.
GN OrderedLocusNames=CAC3619;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1488;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RX DOI=10.1128/JB.136.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC EMBL; AE007858; AAK81542.1; -.
DR FMR; C97344; C97344.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BPD transp.
DR InterPro: IPR010065; HEQRO ABC 3TM.
DR Pfam: PF00528; BPD transp_I; 1.
DR TIGRFAMs: TIGR01726; HEQRO_perm_3TM; 1.
DR PROSITE: PS50928; ABC_TM1; 1.
DR Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 217 AA; 23743 MW; 36738BCDCE9A2F CRC64;

```

Query Match 9.2%; Score 88.5; DB 2; Length 217;
 Best Local Similarity 24.8%; Pred. No. 4.6;
 Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLHACIPQCRGSSNTPLTCORYNASV-----TNSVKGNTAI-----LWTCGLG 62
 DB 4 SSLNKVIPVLDGTRITLLTSCSSIIIGCIIGTIAMFKTSSVKVNLNIGKFTWILRG 63
 QY 63 SLIISLAVFY--LMFLLRKISSEPLKDEF-----KNTGS-----GLIGMANIDLEKR 108
 DB 64 PLLQLQVYVYGPFSLDSKLTWTPKAAIIGLSNLSNGAYIAEIRGILAINDGOPEASK 123
 QY 109 -----TGDEILPRGLETVVEEC-----TCEDCI-KSKPKVDSH 142
 DB 124 ALGLTGQTKWRIILQARVILPPCGNEFIAMIKDTSIVITMEELRKAQLVSSG 183
 QY 143 CFFLPAMERGA--TILVTKTNDYCKSLPAALSATIEKIS 182
 DB 184 DAVTPVLFAGIFVYLLTIFTGIFSK-----IEKLS 215

RESULT 11

Q80XB3 PRELIMINARY; PRT; 804 AA.
 AC Q80XB3;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Prominin-1 t2 isoform.
 GN Name=Prom1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Testis;
 RX PubMed=15316084;
 RA Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.,
 RA Corbeil D.;
 RT "Identification of novel Prominin-1/CD133 splice variants with
 RT alternative C-termini and their expression in epididymis and testis.";
 RL J. Cell Sci. 117:4301-4311(2004).
 DR EMBL; AY223521; AAO72429.1; --
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prominin.
 DR Pfam; PF05478; Prominin; 1.
 SQ SEQUENCE 804 AA; 89983 MW; CFC9D68BCF9FF16 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 804;
 Best Local Similarity 22.7%; Pred. No. 27;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQCRGSSNTPLTCORYNASVTSNKGNTAIWTCGLSLIISLAVFVLMFLL 77
 DB 112 LVGCFPCMCRC-----CNK-CGEMHQKQKQAPCRKCLGSLVLCILMSLGIY 162
 QY 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTD-EIIL---PRGLETVVECTCE--- 129
 DB 163 GFVANQOTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 213
 QY 130 -----DCIKS-----KPKVDSHCFPLPAMEGATILVTK-TNDYCKSLPAAL-- 172
 DB 214 FSDLDGIGSVLGRIKDQPKV-----TPVLEEIKAMATAIKOTDALQNMSSSLKS 266
 QY 173 ---SATEIEKSISA 183
 DB 267 LQDAATQLTNLS 280

RESULT 12

Q80XB2 PRELIMINARY; PRT; 809 AA.
 AC Q80XB2;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Prominin-1 T3 isoform.
 GN Name=Prom1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Testis;
 RX PubMed=15316084;
 RA Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.,
 RA Corbeil D.;
 RT "Identification of novel Prominin-1/CD133 splice variants with
 RT alternative C-termini and their expression in epididymis and testis.";
 RL J. Cell Sci. 117:4301-4311(2004).
 DR EMBL; AY223522; AAO72430.1; --
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prominin.
 DR Pfam; PF05478; Prominin; 1.
 SQ SEQUENCE 809 AA; 90605 MW; BC991E100C623AE1 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 809;
 Best Local Similarity 22.7%; Pred. No. 27;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQCRGSSNTPLTCORYNASVTSNKGNTAIWTCGLSLIISLAVFVLMFLL 77
 DB 117 LVGCFPCMCRC-----CNK-CGEMHQKQKQAPCRKCLGSLVLCILMSLGIY 167
 QY 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRGTD-EIIL---PRGLETVVECTCE--- 129
 DB 168 GFVANQOTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 218
 QY 130 -----DCIKS-----KPKVDSHCFPLPAMEGATILVTK-TNDYCKSLPAAL-- 172
 DB 219 FSDLDGIGSVLGRIKDQPKV-----TPVLEEIKAMATAIKOTDALQNMSSSLKS 271
 QY 173 ---SATEIEKSISA 183
 DB 272 LQDAATQLTNLS 285

RESULT 13

Q80XB6 PRELIMINARY; PRT; 823 AA.
 AC Q80XB6;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Prominin T4 isoform.
 GN Name=Prom1; Synonyms=Prom;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Testis;
 RX PubMed=15316084;
 RA Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.,
 RA Corbeil D.;
 RT "Identification of novel Prominin-1/CD133 splice variants with

RT alternative C-termini and their expression in epididymis and testis";
 RL J. Cell Sci. 117:4301-4311 (2004).
 DR EMBL; AY099088; AAM28245.1; -.
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prolaminin.
 DR Pfam; PF05478; Prolaminin; 1.
 SQ SEQUENCE 823 AA; 92225 MW; 9EF01A18DB84EFAC CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 823;
 Best Local Similarity 22.7%; Pred. No. 28;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSSNPPLTCQRYCNASVTNSVKGTVNAILWTCLGLSLIISLAVFLMFL 77
 DB 117 LVGCGFFCMCR-----CNK-CGGMHQKQKQAPCRKCLGLSLVCLMSLGIY 167

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSRGTD-EIIL---PRGLETVVECTCE--- 129
 DB 168 GFVAHQOTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 218

QY 130 ----DCIKS-----KPKVDSHCHFPFLPAMEGATILVTK-TNDYCKSLPAL-- 172
 DB 219 FSDLDGIGSVLGGRIKQDLKPKV-----TPVLEEIKAMATAIKOTKDALQNMSSLSKS 271

QY 173 ---SATEIEKSISA 183
 DB 272 LQDAATQLNTNLSS 285

RESULT 14
 Q8CDK8 PRELIMINARY; PRT; 827 AA.
 AC Q8CDK8 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:493144ON24 product:prominin, full insert sequence.
 GN Names=Prom1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK029921; BAC26678.1; -.
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prolaminin.
 DR Pfam; PF05478; Prolaminin; 1.
 SQ SEQUENCE 827 AA; 92714 MW; DBCA5ED2DF401A18 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 827;
 Best Local Similarity 22.7%; Pred. No. 28;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSSNPPLTCQRYCNASVTNSVKGTVNAILWTCLGLSLIISLAVFLMFL 77
 DB 117 LVGCGFFCMCR-----CNK-CGGMHQKQKQAPCRKCLGLSLVCLMSLGIY 167

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSRGTD-EIIL---PRGLETVVECTCE--- 129
 DB 168 GFVAHQOTRIKGTQK-----LAKSNFRDFTLLTETPKQIDYVVEQYTNKKA 218

QY 130 ----DCIKS-----KPKVDSHCHFPFLPAMEGATILVTK-TNDYCKSLPAL-- 172
 DB 219 FSDLDGIGSVLGGRIKQDLKPKV-----TPVLEEIKAMATAIKOTKDALQNMSSLSKS 271

QY 173 ---SATEIEKSISA 183
 DB 272 LQDAATQLNTNLSS 285

RESULT 15
 Q8BH12 PRELIMINARY; PRT; 834 AA.
 AC Q8BH12 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 28, Last annotation update)
 DE Prominin T1 isoform (Mus musculus adult male testis cDNA, RIKEN full-
 DE length enriched library, clone:4932416E19 product:prominin, full
 DE insert sequence).

GN Name=Prom1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/c; TISSUE=Testis;
RC PubMed=15316084;
RX Fargass C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B., Corbeil D.;
RA "Identification of novel Prominin-1/CD133 splice variants with alternative C-termini and their expression in epididymis and testis."; J. Cell Sci. 117:4301-4311(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shino H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
[7]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC STRAIN=C57BL/6J; Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Itoh M., Kagawa I., Kasukawa T., Hori F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305215; AA011840.1; -;
DR MGD; AK030027; BAC26745.1; -;
DR MGD; MGI:1100886; Prom1.
DR GO; GO:0005903; C:brush border; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005902; C:microvillus; IDA.
DR InterPro; IPR008795; Prominin.
DR Pfam; PF05478; Prominin; 1.
SQ SEQUENCE 834 AA; 93444 MW; 5ABA26C80F636E45 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 834;
Best Local Similarity 22.7%; Pred. No. 28;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQCLRCSSNTPPLTCQRYCNASVNSVKGNTNAILWTCLGLSLIISLAVFLMFL 77
Db 117 LVGCFPCMCRC-----CNK-CGEMHQKQKQNAPCRRKCLGLSLVLCILMSLGIY 167
QY 78 KXISSEPLKDBFKNTGSGLLGMANIDLEKSRGTD-EIIL---PRGLETVVECTCE---- 129
Db 168 GFVANQQTTRTRIKGTOK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNKKA 218
QY 130 ----DCIKS-----KPKVDSHCHFPPLPAMEEGATILVTK-TNDYCKSLPAAL-- 172
Db 219 FSDLDCIGSVLGGRIKDKLPKV-----TPVLEIKAMATAIKQTKDALQNMSSLSKS 271
QY 173 ---SATEIEKSISA 183
Db 272 LQDAATQLNTNLSS 285

Search completed: February 26, 2005, 21:00:48
Job time : 178.953 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:45:33 ; Search time 10.634 Seconds
(without alignments)
461.448 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 283
Sequence: 1 MLQMAQCQSQNEYFDSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	184	S43486	B-cell maturation factor - human
2	70.5	24.9	1548	S34583	serine proteinase
3	69.5	24.6	5376	T42215	zonadhesin - mouse
4	68.5	24.2	1101	T16840	hypothetical prote
5	65.5	23.1	1299	T43251	furin (EC 3.4.21.7
6	62.5	22.1	999	T19275	hypothetical prote
7	62	21.9	330	T25169	hypothetical prote
8	61.5	21.7	99	S60231	gibberellin-regula
9	61.5	21.7	493	T24856	hypothetical prote
10	61.5	21.7	520	G88846	protein fl2A7.2 [l
11	60.5	21.4	1574	T13954	MEGF6 protein - ra
12	60.5	21.4	3034	T14119	seven-pass transme
13	59.5	21.0	388	T31887	hypothetical prote
14	59.5	21.0	388	T31888	hypothetical prote
15	59.5	21.0	438	T31889	hypothetical prote
16	59.5	21.0	445	T31898	hypothetical prote
17	59	20.8	758	T15577	epidermal growth f
18	59	20.8	1717	A45558	alpha-51D immobili
19	58.5	20.7	2533	T28675	alpha-51D-immobili
20	58.5	20.7	2533	T28674	chymotrypsin/elast
21	58	20.5	63	S07127	hypothetical prote
22	58	20.5	1513	T23681	hypothetical prote
23	58	20.5	1816	S68960	laminin alpha-4 ch
24	57.5	20.3	1680	A43434	furin (EC 3.4.21.7
25	57	20.1	502	T20130	hypothetical prote
26	57	20.1	653	T20130	hypothetical prote
27	57	20.1	838	T20125	hypothetical prote
28	56.5	20.0	701	S62460	hypothetical prote
29	56	19.8	2476	T34022	zonadhesin - pig

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidir
A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <LA>
A;Cross-references: UNIPROT:Q02223; EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA>
A;Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:g29408
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 283; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQCQSQNEYFDSLHACIPQCRLCSNTPPLTCQRYCNASVTNSVKG 51
Db 1 MLQMAQCQSQNEYFDSLHACIPQCRLCSNTPPLTCQRYCNASVTNSVKG 51

RESULT 2

S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S34583
R;Nakagawa, T.; Murakami, K.

FEBS Lett. 327, 165-171, 1993

A/Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a

A/Reference number: S34583; MUID:93327934; PMID:8335106

A/Accession: S34583

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1548 <NAK>

A/Cross-references: UNIPROT:Q04592; GB:D17583; NID:g07344; PIDN:BAA04507.1; PID:d100503

C/Keywords: hydrolase; serine proteinase

Query Match **24.98;** Score 70.5; DB 2; Length 1548;
Best Local Similarity 34.7%; Pred.No. 4.1;
Matches 1; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

RESULT 3
T42215
zonadhesin - mouse
N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42215

R/Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
 A>Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
 A|Reference number: Z22080; MUID:98123114; PMID:9542463
 A|Accession: T42215
 A|Status: preliminary; translated from GB/EMBL/DBDJ
 A|Molecule type: mRNA
 A|Residues: 1-5376 <GAO>

A:Map position: 5
C:Function:
A:Description: functions in multiple cell adhesion processes
A:Note: found exclusively on the apical region of the sperm head
C:Keywords: cell adhesion

[illegible]

RESULT 4
Tl6840
Hypothetical protein Tl0E10.4 - *Caenorhabditis elegans*
CfSpecies: *Caenorhabditis elegans*
CfDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CfAccession: Tl6840
R:Geisel, C.
Submitted to the EMBL Data Library, October 1995
A>Description: the sequence of *C. elegans* cosmid Tl0E10.

A:Reference number: Z18588
A:Accession: T1840
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA803
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP.T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 24.2%; Score 68.5; DB 2; Length 1101;

[illegible]

```

RESULT 5
T43251
furin (EC 3.4.21.75) - fall armyworm
N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C/Species: Spodoptera frugiperda (fall armyworm)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43251

```

R; Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A; Description: Cloning and functional characterization of FURIN from *Spodoptera frugiper*
A; Reference number: Z22368
A; Accession: T43251
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-1299 <CIE>

A;Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:g1167859; PID:e219690; PIDN:CAA9311
A;Experimental source: clone Sfurin 6; ovary
C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specific
C;Keywords: hydrolase; serine proteinase

```
Query Match      23.1%; Score 65.5; DB 2; Length 1299;
Best Local Similarity 34.0%; Pred. No. 13;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;
```

QY 8 CSQNEYFDSLHACIPCOLRCS-----SNTPELTCCRYCNAS-----VTNSVKG 51
||| : ||| : ||| : |||
db 1150 CGRPLRIDRLNNQCVC---CSEGVGTSTPTPDC-CHCNPGENGCSINVAG 1198

RESULT 6
T19275
hypothetical protein F34D10.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19275; T21723
R;Harris, B.

submitted to the EMBL Data Library, September 1994
A; Reference number: Z19099
A; Accession: T19275
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-999 <WIL>
A; Cross-references: UNIPROT: Q17969; EMBL: Z37139; PIDN: CAA85494.1; GSPDB: GNO0021; CESP: F31481
A; Experimental source: clone C1481

R:Kershaw, J.
 Submitted to the EMBL Data Library, June 1994
 A:Reference number: Z19464
 A:Accession: T21723
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-999 «W12»
 A:Cross-references: EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GNC00021; CESP:F34D10.2

A:Experimental source: clone F34D10
C:Genetics:
A;Gene: CESP:F34D10.2
A;Map position: 3
A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870/

Query Match 22.1%; Score 62.5; DB 2; Length 999;
Best Local Similarity 42.5%; Pred. No. 23;
Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 13 YPDSLHACIQL-RCSNTPPLTTCQRYCNASVTNSVKG 51
 ||||| :||| :|||

A:Accession: T24856
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-483 <WIL>
A:Cross-references: UNIPROT:Q22423; EMBL:Z73911; PIDN:CAA98142.2; GSPDB:GN00022; CESP:T
A:Experimental source: clone T12A7
C:Genetics:
A:Gene: CESP:T12A7.2
A:Map position: 4
A:Introns: 36/3; 71/1, 146/1, 255/2; 287/2; 340/3; 387/1; 449/2

Query Match 21.7%; Score 61.5; DB 2; Length 483;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 108 CMNDGYFNHTLGRCV-----CTSNWVGEHCIFRCNSGVVNTSG 146

RESULT 10
G88846
protein T12A7.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88846
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.el
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A:Accession: G88846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <STO>
A:Cross-references: UNIPROT:Q22423; GB:chr_IV; PIDN:CAA98142.1; PID:g3879789; GSPDB:GN0
C:Genetics:
A:Gene: T12A7.2
A:Map position: 4

Query Match 21.7%; Score 61.5; DB 2; Length 520;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 145 CMNDGYFNHTLGRCV-----CTSNWVGEHCIFRCNSGVVNTSG 183

RESULT 11
Tl3954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Tl3954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: Tl3954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 21.4%; Score 60.5; DB 2; Length 1574;
Best Local Similarity 32.2%; Pred. No. 56;
Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 20:57:04 ; Search time 13.0213 Seconds
(without alignments)
292.376 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 283
Sequence: 1 MLQMGCCSQNEYFDSLHACIPQRCSSNTPPLTCQRYCNASVTNSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	100.0	184	4	US-09-565-423-11
2	283	100.0	152	4	US-09-949-016-11115
3	269	95.1	51	4	US-09-854-864-6
4	269	95.1	181	4	US-09-854-864-5
5	269	95.1	283	4	US-09-854-864-9
6	249	88.0	58	4	US-09-854-864-21
7	201	71.0	34	4	US-09-854-864-7
8	201	71.0	81	4	US-09-854-864-13
9	181	64.0	185	4	US-09-565-423-17
10	181	64.0	185	4	US-09-854-864-11
11	181	64.0	281	4	US-09-854-864-10
12	104	36.7	117	4	US-09-854-864-12
13	67.5	23.9	59	4	US-09-854-864-20
14	67.5	23.9	166	2	US-08-810-572A-6
15	67.5	23.9	166	3	US-09-290-333-6
16	67.5	23.9	166	4	US-09-782-857A-6
17	67.5	23.9	166	4	US-09-854-864-15
18	67.5	23.9	293	2	US-08-810-572A-2
19	67.5	23.9	293	3	US-09-290-333-2
20	67.5	23.9	293	4	US-09-782-857A-2
21	67.5	23.9	293	4	US-09-879-919-22
22	67.5	23.9	293	4	US-09-848-295-4
23	67.5	23.9	293	4	US-09-854-864-14
24	67.5	23.9	397	4	US-09-854-864-18
25	66.5	23.5	67	4	US-09-854-864-16
26	63	22.3	1106	4	US-09-949-016-9626
27	59	20.8	556	4	US-09-252-991A-18110

28 58.5 20.7 670 4 US-09-270-767-41037 Sequence 41037, A
29 58.5 20.7 670 4 US-09-270-767-56253 Sequence 56253, A
30 58 20.5 1792 4 US-09-561-818A-4 Sequence 4, Appli
31 58 20.5 1800 4 US-09-561-818A-8 Sequence 8, Appli
32 58 20.5 1816 4 US-09-561-818A-2 Sequence 2, Appli
33 58 20.5 1824 4 US-09-561-818A-6 Sequence 6, Appli
34 57.5 20.3 142 4 US-09-848-295-2 Sequence 2, Appli
35 57 20.1 201 4 US-09-270-767-31650 Sequence 31650, A
36 57 20.1 201 4 US-09-270-767-46867 Sequence 46867, A
37 57 20.1 760 4 US-09-589-8928-11 Sequence 11, Appli
38 56 19.8 2476 2 US-08-276-967-2 Sequence 2, Appli
39 55.5 19.6 3647 3 US-09-949-016-10932 Sequence 10932, A
40 55.5 19.6 5405 3 US-08-718-388-9 Sequence 9, Appli
41 55 19.4 142 4 US-09-270-767-56958 Sequence 56958, A
42 55 19.4 392 4 US-09-270-767-41714 Sequence 41714, A
43 55 19.4 991 4 US-09-902-540-11984 Sequence 11984, A
44 55 19.4 1792 4 US-09-561-818A-12 Sequence 12, Appli
45 55 19.4 1816 4 US-09-561-818A-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQMGCCSQNEYFDSLHACIPQRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 1 MLQMGCCSQNEYFDSLHACIPQRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 2
US-09-949-016-11115
; Sequence 11115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11115

Query Match 100.0%; Score 283; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 3.5e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 9 MLQWAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 59

RESULT 3
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 95.1%; Score 269; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.9e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

RESULT 4
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 95.1%; Score 269; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

RESULT 5
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 95.1%; Score 269; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48

RESULT 6
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 88.0%; Score 249; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 44

RESULT 9
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:

```
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match          64.0%; Score 181; DB 4; Length 185;
Best Local Similarity 70.8%; Pred.No. 4.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4   MAGQCSONEYFDSLHACIPQLCRCSNTPPLTCQRCYNASVTNSVKG 51
         ||| :|||:|||:|||||:|||||:|||||:|||||:|||||:
Db       1   MAQQCFHSEYFDLSLHACKPCHLRCSN--PPATCQPCDPSVTSVKG 46

RESULT 10
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match          64.0%; Score 181; DB 4; Length 185;
Best Local Similarity 70.8%; Pred.No. 4.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4   MAGQCSONEYFDSLHACIPQLCRCSNTPPLTCQRCYNASVTNSVKG 51
         ||| :|||:|||:|||||:|||||:|||||:|||||:|||||
Db       1   MAQQCFHSEYFDLSLHACKPCHLRCSN--PPATCQPCDPSVTSVKG 46

RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
```


Query Match 23.9%; Score 67.5; DB 3; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy 8 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRVCA 43
| : | : | : | : | : | : | : | :
Db 34 CPBEEYWDPLLGTMSCKTICNHQS-QRTCAAFCRS 68

Search completed: February 26, 2005, 21:06:29
Job time : 14.0213 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:24:52 ; Search time 54.0383 Seconds
(without alignments)
365.015 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 283

Sequence: 1 MLCMAGCQSQNEVFDLLHA.....TPPLTCQRYCNASVNSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	184	3 AAB08843	Aab08843 Amino aci
2	283	100.0	184	3 AAY94001	Aay94001 A human B
3	283	100.0	184	4 AAE09241	Aae09241 Human BCM
4	283	100.0	184	4 AAY71979	Aay71979 Human B C
5	283	100.0	184	4 AAB60698	Aab60698 Human BAF
6	283	100.0	184	4 AAE00506	Aae00506 Human B C
7	283	100.0	184	5 ABB81487	Abb81487 Human BCM
8	283	100.0	184	5 ABP54694	Abp54694 Metastati
9	283	100.0	184	5 AAE28961	Aae28961 Human B-c
10	283	100.0	184	6 AAE35216	Aae35216 Human B-c
11	283	100.0	184	6 ADA9361	Ada9361 Human BCM
12	283	100.0	184	6 ABP60552	Abp60552 Human tum
13	283	100.0	184	6 ABP97717	Abp97717 Amino aci
14	283	100.0	184	7 ADD67527	Add67527 Human Lvl
15	283	100.0	184	7 ADG43715	Adg43715 Human B-c
16	283	100.0	184	8 ADK00756	Adk00756 Native hu
17	283	100.0	184	8 ADQ94442	Adq94442 Neutrokin
18	283	100.0	184	8 ADP56014	Adp56014 Human PRO
19	283	100.0	302	4 AAB60699	Aab60699 Mouse IGG
20	283	100.0	302	4 AAE00507	Aae00507 Human BCM
21	283	100.0	302	7 ADG43717	Adg43717 Human B-c
22	277	97.9	184	6 ABR40082	Abr40082 Human Gen
23	274	96.8	288	5 ABG95060	Abg95060 Human tra
24	269	95.1	51	5 AAE15485	Aae15485 Human B-c
25	269	95.1	181	5 AAE15484	Aae15484 Human B-c

26	269	95.1	283	5 AAE15488	Aae15488 Human BCM
27	249	88.0	58	5 AAE15501	Aae15501 Human B C
28	206	72.8	157	4 AAB60700	Aab60700 Human BAF
29	201	71.0	34	5 AAE15486	Aae15486 Human B-c
30	201	71.0	34	6 ADA9366	Ada9366 Human BCM
31	181	64.0	185	3 AAB08844	Aab08844 Amino aci
32	181	64.0	185	4 AAY71980	Aay71980 Murine B
33	181	64.0	185	5 AAE15490	Aae15490 Mouse B C
34	181	64.0	281	5 AAE15489	Aae15489 Mouse BCM
35	158	55.8	42	6 ABJ38417	Abj38417 TALL-1 re
36	151	53.4	26	7 ADI53060	Adi53060 Human BCM
37	104	36.7	117	5 AAE15491	Aae15491 Human-mur
38	90.5	32.0	24	5 AAE15492	Aae15492 Human-mur
39	71.5	25.3	249	3 AAY94006	Aay94006 A murine
40	71.5	25.3	249	7 ABM85744	Abm85744 Mouse pro
41	70.5	24.9	1548	7 ADC71568	Adc71568 Mouse sub
42	70.5	24.9	1877	7 ABB80243	Abb80243 Murine su
43	68.5	24.2	332	6 AAE35228	Aae35228 Human TAC
44	68.5	24.2	1569	8 ADRI8921	Adri8921 Human muc
45	68.5	24.2	2240	8 ADRI8914	Adri8914 Mature Hu

ALIGNMENTS

RESULT 1

AAB08843

ID AAB08843 standard; peptide; 184 AA.

AC AAB08843;

XX

DT 02-JAN-2001 (first entry)

XX

DE Amino acid sequence of human.

XX

KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
anti-cell death gene; apoptosis; viral infection; inflammatory response;
rheumatoid arthritis; inflammatory bowel disease; septic shock.

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Domain 57. .77

FT /note= "putative transmembrane domain"

XX WO200050633-A1.

XX

PD 31-AUG-2000.

XX

PF 24-FEB-2000; 2000WO-US004925.

XX

PR 24-FEB-1999; 99US-0121485P.

XX

PA (GENO) GEN HOSPITAL CORP.

XX

PI Seed B, Ting A;

XX WPI; 2000-558405/51.

DR

XX

PT Identifying a modulator of gene expression for drug designing, by

PT contacting a compound library with a cell expressing an anti-cell death

PT gene and reporter gene, and determining alteration in reporter gene

PT expression.

XX

PS Claim 32; Fig 7A; 53pp; English.

XX

CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is

CC a necrosis factor (NF)-kB activator. The method of the invention is used

CC to identify compounds which modulate BCMA activity (and thus NF-kB

CC activity). The specification describes a method of identifying a

CC polypeptide which increases gene expression from a promoter. The method

CC involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to

CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51
 |||||
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 2
 AAY94001
 ID AAY94001 standard; protein; 184 AA.
 XX
 AC AAY94001;

DT 20-OCT-2000 (first entry)

DE A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO200040716:A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI: 2000-452538/39.

XX N-PSDB; AAY58559.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated

CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51
 |||||
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 3

AAE09241

ID AAE09241 standard; protein; 184 AA.

XX AAE09241;

DT 19-NOV-2001 (first entry)

DE Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0226986P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 XX Yan M;

XX WPI: 2001-541628/60.

XX N-PSDB; AAD15902.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.

XX Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating

The present invention relates to Tumour necrosis factor (TNF) and Apol- related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in- particular relates to methods for regulating the interaction between TALL- 1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE) insulin dependent diabetes mellitus, multiple

AA The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFF-R is a member of
CC

CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAFF-R
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51

RESULT 6
 AAE00506
 ID AAE00506 standard; protein; 184 AA.
 XX
 AC AAE00506;
 DT 31-JUL-2001 (first entry)
 XX
 DE Human B cell maturation protein (BCMA).

XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCW; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;
 KW tumour necrosis factor; BCMA; B cell maturation protein.

XX Homo sapiens.
 XX WO200124811-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000WO-US027579.
 XX 06-OCT-1999; 99US-0157933P.
 XX 11-FEB-2000; 2000US-0181807P.
 XX 30-JUN-2000; 2000US-0215688P.
 XX (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 XX WPI; 2001-266242/27.
 XX N-PSDB; AAD03844.
 XX

PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 PT antagonist.

XX Claim 3; Fig 3A; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition
 PS associated with undesired cell proliferation such as cancer or carcinoma.
 XX The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCW or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is human APRIL-R also referred as BCMA or BCM protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51

RESULT 7
 ABB81487
 ID ABB81487 standard; protein; 184 AA.
 XX
 AC ABB81487;
 DT 02-SEP-2002 (first entry)
 XX
 DE Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.
 XX WO200238766-A2.
 XX 16-MAY-2002.
 XX 05-NOV-2001; 2001WO-US047018.
 XX 07-NOV-2000; 2000US-0246449P.
 XX 20-DEC-2000; 2000US-0257131P.
 XX 28-JUN-2001; 2001US-0301715P.
 XX 29-AUG-2001; 2001US-0315565P.

XX (ZYMO) ZYMOGENETICS INC.
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 XX WPI; 2002-508212/54.
 XX

PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Znf12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.

XX Disclosure; Page 135-136; 154pp; English.

XX
 CC The present invention describes a human tumour necrosis factor receptor
 CC designated Znf12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Znf12
 CC (e.g. ZNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGCCSQNEVFDLSLLHACIPCLQRCSSNTPLTCQRYCNASVTNSVKG 51
 DB 1 MLQMGCCSQNEVFDLSLLHACIPCLQRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 8
 ABP54694

ID ABP54694 standard; protein; 184 AA.

XX AC ABP54694;

XX DT 30-DEC-2002 (first entry)

XX DE Metastatic colorectal cancer-associated polypeptide.

XX KW Colorectal cancer; metastasis; differential expression; cytostatic;
 KW diagnosis; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200268677-A2.

XX PD 06-SEP-2002.

XX PF 27-FEB-2002; 2002WO-US006001.

XX PR 27-FEB-2001; 2001US-0272206P.

XX PR 02-APR-2001; 2001US-0281149P.

XX PR 17-APR-2001; 2001US-0284555P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX PI Mack DH, Markowitz SD;

XX DR WPI; 2002-698677/75.

XX DR N-PSDB; ABQ81560.

XX

PT New genes that are up- or down-regulated in colorectal cancer, useful for
 PT diagnosing colorectal cancer in a subject, or for identifying modulators
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.

XX Claim 8; Page 255; 260pp; English.

XX
 CC The present sequence is the protein sequence of a human polypeptide
 CC encoded by a gene that exhibits decreased expression in colon cancer-
 CC derived metastases compared to normal colon tissue. It is an example of
 CC claimed polypeptides that are encoded by genes which are differentially
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are
 CC useful in diagnostic and prognostic assays, for raising antibodies useful
 CC e.g. in immunotherapy, and in screening for modulator compounds of
 CC therapeutic value

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGCCSQNEVFDLSLLHACIPCLQRCSSNTPLTCQRYCNASVTNSVKG 51

DB 1 MLQMGCCSQNEVFDLSLLHACIPCLQRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 9

AAE28961

ID AAE28961 standard; protein; 184 AA.

XX AC AAE28961;

XX DT 27-JAN-2003 (first entry)

XX DE Human B-cell maturation antigen (BCMA).

XX KW Human; tumour; B-cell maturation antigen; transmembrane activator;
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 KW BCMA; multiple myeloma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..54 "Antigenic epitope"

FT Domain 1..48

FT Region 8..41 "Extracellular domain"

FT Region 8..41 "Cysteine rich region"

XX PN WO200266516-A2.

XX PD 29-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003500.

XX PR 20-FEB-2001; 2001US-0270274P.

XX PR 12-APR-2001; 2001US-0283447P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kindevogel W;

XX DR WPI; 2002-723183/78.

XX DR N-PSDB; AAD46410.

XX KW B-cell maturation antigen and transmembrane activator and calcium-
 KW modulator and cyclophilin ligand-interactor, useful for treating
 KW disorders e.g. inflammation or lymphoma.

XX

PS Disclosure; Page 63; 67pp; English.

XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC TGNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasia, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein

XX Sequence 184 AA;

Query Match 100.0%; Score 283; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOWAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

Db 1 MLOWAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 10

AAE35216

ID AAE35216 standard; protein; 184 AA.

XX AAE35216;

XX 28-MAY-2003 (first entry)

XX Human B-cell maturation receptor (BCMA) protein.

XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW B-cell maturation receptor; BCMA; receptor.

XX Homo sapiens.

XX WO200294852-A2.

XX 28-NOV-2002.

XX 20-MAY-2002; 2002WO-US015910.

XX 24-MAY-2001; 2001US-0293343P.

XX (ZYMO) ZYMOGENETICS INC.

XX Rixon MW, Gross JA;

XX WPI; 2003-148455/14.

XX N-PSDB; AAE353754.

XX Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

PS Disclosure; Col 100; 71pp; English.

XX The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for

CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human B-cell maturation receptor
CC (BCMA) protein used in the invention

XX Sequence 184 AA;

Query Match 100.0%; Score 283; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOWAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

Db 1 MLOWAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 11

ADA9361

ID ADA9361 standard; protein; 184 AA.

XX ADA9361;

XX 20-NOV-2003 (first entry)

XX Human BCMA protein.

XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
KW antiinflammatory; antiarthritic; dermatological; antidiabetic;
KW neuroprotective; antithyroid; antipruritic; nephrotropic; vasotropic;
KW vaccine; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
KW multiple sclerosis; myasthenia gravis; Grave's disease;
KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

OS Homo sapiens.

XX WO2003035846-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

XX 14-JAN-2002; 2002US-0348962P.

XX 07-FEB-2002; 2002US-0354966P.

XX 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX N-PSDB; ADA9360.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.

XX Claim 62; Page 613; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting abgr; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,

CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarthritis nodosa. The present sequence represents human BCMA.
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSNTPLTCORYCNASVTNSVKG 51
 DB 1 MLQWAGCQSQNEYFDSLHACIPQLRCSNTPLTCORYCNASVTNSVKG 51

RESULT 12

ABP60552
 ID ABP60552 standard; protein; 184 AA.

XX AC ABP60552;

XX DT 28-MAR-2003 (first entry)

XX DE Human tumour necrosis factor BCMA.

XX KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
 KW antiarthritic; cytostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculosic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.

XX OS Homo sapiens.

XX PN WO20294192-A2.

XX PD 28-NOV-2002.

XX PF 22-MAY-2002; 2002WO-US016106.

XX PR 24-MAY-2001; 2001US-0293100P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM;

XX DR WPI; 2003-156740/15.

XX PT Novel isolated antibody that immunospecifically binds tumor necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.

XX PS Disclosure; Page 222; 225pp; English.

XX CC The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 CC antiallergic, antidiabetic, neuroprotective, ophthalmological,
 CC tuberculosic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in

CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosic, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor BCMA
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSNTPLTCORYCNASVTNSVKG 51
 DB 1 MLQWAGCQSQNEYFDSLHACIPQLRCSNTPLTCORYCNASVTNSVKG 51

RESULT 13

ABP97717

ID ABP97717 standard; protein; 184 AA.

XX AC ABP97717;

XX DT 28-MAY-2003 (first entry)

XX DE Amino acid sequence of human BCMA receptor.

XX KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus; BCMA.

XX OS Homo sapiens.

XX PN WO2003014294-A2.

XX PD 20-FEB-2003.

XX PF 24-JUL-2002; 2002WO-US023487.

XX PR 03-AUG-2001; 2001US-0310114P.

XX PR 30-APR-2002; 2002US-0377171P.

XX PA (GETH) GENENTECH INC.

XX PI Dixit V, Grewal I, Ridgway J, Yan M;

XX DR WPI; 2003-256560/25.

XX DR N-PSDB; ABZ68871.

XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.

XX PS Disclosure; Fig 2; 153pp; English.

XX CC The present sequence represents a human BCMA polypeptide. The
 CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 14
ADD67527
ID ADD67527 standard; protein; 184 AA.
XX AC ADD67527;
XX DT 15-JAN-2004 (first entry)
XX DE Human Ly1732P protein SEQ ID NO:4.
XX KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
KW vaccine; immunotherapy; cancer; multiple myeloma cell;
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
human.
XX OS Homo sapiens.
XX PN WO2003062401-A2.
XX PD 31-JUL-2003.
XX PF 22-JAN-2003; 2003WO-US002353.
XX PR 22-JAN-2002; 2002US-00057475.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordenez N;
PI Carter L, McNeill PD;
XX WPI; 2003-598749/56.
XX N-PSDB; ADD67526.
XX PT New hematological malignancy-related genes and polypeptides, useful for
PT screening anti-cancer agents, and generating antibodies or
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT lymphocytic leukemia.
XX PS Claim 9; SEQ ID NO 4; 307pp; English.
XX CC The present invention describes an isolated polynucleotide (1), which is
CC overexpressed in haematological malignancies, and which encodes a
CC polypeptide or an immunogenic fragment of the polypeptide. Also
CC described: (1) an isolated polypeptide; (2) an expression vector
CC comprising (1) operably linked to an expression control sequence; (3) a
CC host cell comprising an expression vector; (4) an isolated antibody that
CC specifically binds to the polypeptide or its immunogenic fragment; and
CC (5) immunoconjugates comprising the antibody above, or an antibody that
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC by (1). (1) has cytostatic and immunostimulant activities, and can be
CC used in vaccines and immunotherapy. The immunoconjugates are useful in
CC the manufacture of a medicament, particularly as active ingredients in a
CC composition for treating cancer, e.g. multiple myeloma cell, chronic
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC The polynucleotide (1) or polypeptide can be used for screening anti-
CC cancer agents, and generating antibodies or immunoconjugates for treating
CC or preventing the above-mentioned diseases. The polynucleotide,
CC polypeptide or antibody can be used for detecting, diagnosing or
CC prognosticating the haematological malignancies described above. The
CC present sequence is used in the exemplification of the present invention.
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 15
ADG43715
ID ADG43715 standard; protein; 184 AA.
XX AC ADG43715;
XX DT 26-FEB-2004 (first entry)
XX DE Human B-cell maturation antigen SEQ ID NO:1.

XX KW human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
gene therapy.
XX OS Homo sapiens.

XX PN WO2003072713-A2.
XX PD 04-SEP-2003.
XX PF 21-FEB-2003; 2003WO-US005147.
XX PR 21-FEB-2002; 2002US-0358427P.
XX PA (BIOJ) BIOGEN INC.

XX PI Kalled SL, Reid H;
XX WPI; 2003-721758/68.
XX N-PSDB; ADG43716.

XX PT Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

XX PS Claim 8; Page 68-69; 72pp; English.

XX CC The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nootropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence represents human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51

Search completed: February 26, 2005, 20:45:21
Job time : 54.0383 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:41:13 ; Search time 38.6298 Seconds
(without alignments)
433.092 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	283	100.0	184	13	US-10-077-438-7
3	283	100.0	184	13	US-10-077-137-1
4	283	100.0	184	13	US-10-077-137-7
5	283	100.0	184	14	US-10-068-725-2
6	283	100.0	184	14	US-10-151-882-47
7	283	100.0	184	14	US-10-115-192-8
8	283	100.0	184	14	US-10-008-063-7
9	283	100.0	184	14	US-10-152-363A-27
10	283	100.0	184	14	US-10-216-074-11
11	283	100.0	184	15	US-10-087-080-39
12	283	100.0	302	14	US-10-115-192-12
13	269	95.1	51	9	US-09-854-864-6

14	269	95.1	51	9	US-09-855-158-6	Sequence 6, Appli
15	269	95.1	181	9	US-09-854-864-5	Sequence 5, Appli
16	269	95.1	181	9	US-09-855-158-5	Sequence 5, Appli
17	269	95.1	283	9	US-09-854-864-9	Sequence 9, Appli
18	269	95.1	283	9	US-09-855-158-9	Sequence 9, Appli
19	263	92.9	207	13	US-10-077-438-3	Sequence 3, Appli
20	263	92.9	207	13	US-10-077-137-3	Sequence 3, Appli
21	249	88.0	58	9	US-09-854-864-21	Sequence 21, Appli
22	249	88.0	58	9	US-09-855-158-21	Sequence 21, Appli
23	201	71.0	34	9	US-09-854-864-7	Sequence 7, Appli
24	201	71.0	34	9	US-09-855-158-7	Sequence 7, Appli
25	201	71.0	81	9	US-09-854-864-13	Sequence 13, Appli
26	201	71.0	81	9	US-09-855-158-13	Sequence 13, Appli
27	181	64.0	185	9	US-09-854-864-11	Sequence 11, Appli
28	181	64.0	185	9	US-09-855-158-11	Sequence 11, Appli
29	181	64.0	185	14	US-10-216-074-17	Sequence 17, Appli
30	181	64.0	281	9	US-09-854-864-10	Sequence 10, Appli
31	181	64.0	281	9	US-09-855-158-10	Sequence 10, Appli
32	158	55.8	42	14	US-10-145-206-197	Sequence 197, Appl
33	104	36.7	117	9	US-09-855-158-12	Sequence 12, Appli
34	104	36.7	117	9	US-09-855-158-12	Sequence 12, Appli
35	71.5	25.3	249	13	US-10-087-192-1647	Sequence 1647, Ap
36	70.5	24.9	1568	14	US-10-180-903-2	Sequence 2, Appli
37	69.5	24.6	5374	15	US-10-028-248A-75	Sequence 75, Appli
38	69.5	24.6	5374	15	US-10-107-782-75	Sequence 75, Appli
39	69.5	24.6	5376	15	US-10-028-248A-74	Sequence 74, Appli
40	69.5	24.6	5376	15	US-10-107-782-74	Sequence 74, Appli
41	68.5	24.2	332	14	US-10-152-363A-62	Sequence 62, Appli
42	67.5	23.9	37	9	US-09-779-050A-45	Sequence 45, Appli
43	67.5	23.9	59	9	US-09-854-864-20	Sequence 20, Appli
44	67.5	23.9	59	9	US-09-855-158-20	Sequence 20, Appli
45	67.5	23.9	166	9	US-09-854-864-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 100.0%; Score 283; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 2
US-10-077-438-7
Sequence 7, Application US/10077438
Publication No. US20020165156A1
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Raff S.A.
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
US-10-077-438-7

[illegible]

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RESULT 3
US/10/077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baif Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 184
;
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1
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RESULT 4
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

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RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2
Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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RESULT 6
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|

RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
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Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|

RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
|

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
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FILE REFERENCE: 2003-03-12
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 11
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-216-074-11

Query Match 100.0%; Score 283; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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Db 1 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
|||||

RESULT 11
US-10-087-080-39
Sequence 39, Application US/10087080
Publication No. US20030235820A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Markowitz, Sanford David
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Case Western Reserve University
TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal Cancer
TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
FILE REFERENCE: 018501-000840US
CURRENT APPLICATION NUMBER: US/10/087,080
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/272,206
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US 60/281,149
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/284,555
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 39
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match 100.0%; Score 283; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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Db 1 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
|||||

RESULT 12
US-10-115-192-12
Sequence 12, Application US/10115192
Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof

FILE REFERENCE: A083PCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/215688
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/157933
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 302
TYPE: PRT
ORGANISM: homo sapiens
US-10-115-192-12

Query Match 100.0%; Score 283; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
|||||
Db 24 MLQAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 74
|||||

RESULT 13
US-09-854-864-6
Sequence 6, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: Blys/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In version 3.1
SEQ ID NO 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 95.1%; Score 269; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
|||||
Db 1 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48
|||||

RESULT 14
US-09-855-158-6
Sequence 6, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, B
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27

Search completed: February 26, 2005, 21:04:28
Job time : 38.6298 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 20:37:33 ; Search time 49.0468 Seconds
(without alignments)
532.472 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 283
Sequence: 1 MLQAGQCSQNYFDSLLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	283	100.0	184	1	TR17_HUMAN	Q02223 homo sapien
2	283	100.0	184	2	Q6PE46	Q6pe46 homo sapien
3	181	64.0	185	1	TR17_MOUSE	Q88472 mus musculus
4	73	25.8	718	2	Q9B107	Q9b107 entamoeba h
5	72.5	25.6	499	2	Q88714	Q88714 mus musculus
6	72.5	25.6	1674	2	Q80218	Q80218 mus musculus
7	72.5	25.6	2850	2	Q80703	Q80703 mus musculus
8	71.5	25.3	249	1	T13X_MOUSE	Q9et35 mus musculus
9	71	25.1	3005	2	Q6BFG4	Q6bfg4 paramesium
10	70.5	24.9	1877	1	PKC5_MOUSE	Q04592 mus musculus
11	70	24.7	1025	2	Q7R6J7	Q7r6j7 giardia lam
12	69.5	24.6	5374	2	Q99ND0	Q99nd0 mus musculus
13	69.5	24.6	5376	1	ZAN_MOUSE	Q88799 mus musculus
14	68.5	24.2	966	2	Q22378	Q22378 caenorhabdi
15	68.5	24.2	1569	2	Q6W4X9	Q6w4x9 homo sapien
16	67.5	23.9	233	1	T13X_HUMAN	Q14836 homo sapien
17	67	23.7	532	2	O17496	O17496 ascaris suu
18	65.5	23.1	1299	2	Q26489	Q26489 spodoptera
19	65	23.0	2551	1	SN2_HUMAN	Q8wwg8 h stabilin
20	64.5	22.8	880	2	Q8NAU9	Q8nau9 homo sapien
21	64.5	22.8	880	2	Q8NAU9	Q8nau9 homo sapien
22	64.5	22.8	932	2	Q86U29	Q86u29 homo sapien
23	64.5	22.8	933	2	Q8IX30	Q8ix30 homo sapien
24	64	22.6	494	2	Q729F0	Q729f0 desulfovibr
25	63.5	22.4	548	2	Q9GQ45	Q9gq45 giardia lam
26	63.5	22.4	827	2	Q68FG9	Q68fg9 mus musculus
27	63.5	22.4	933	2	Q66PY1	Q66py1 mus musculus
28	63	22.3	175	1	T13C_MOUSE	Q9d8d0 mus musculus
29	63	22.3	175	2	Q8R4W8	Q8r4w8 mus musculus
30	63	22.3	289	2	Q678B7	Q678b7 lymphocysti
31	63	22.3	341	2	Q6P233	Q6p233 mus musculus

32	63	22.3	341	2	Q8CFA7	Q8cfa7 mus musculus
33	63	22.3	341	2	Q9D351	Q9d351 mus musculus
34	62.5	22.1	985	2	Q8IZ06	Q8iz06 homo sapien
35	62.5	22.1	985	2	Q7Z5T8	Q7z5t8 homo sapien
36	62.5	22.1	999	2	O17969	O17969 caenorhabdi
37	62	21.9	330	2	O18118	O18118 caenorhabdi
38	62	21.9	1592	1	SORL_CHICK	Q98930 g sortilin-
39	62	21.9	3622	2	Q6BG85	Q6bg85 paramesium
40	61.5	21.7	99	1	GAS3_ARATH	P46887 arabidopsis
41	61.5	21.7	353	2	Q8SZ58	Q8sz58 drosophila
42	61.5	21.7	353	2	Q9VW81	Q9vw81 drosophila
43	61.5	21.7	483	2	Q22423	Q22423 caenorhabdi
44	61.5	21.7	798	2	Q9VTR9	Q9vtr9 drosophila
45	61	21.6	247	2	Q7Z6F5	Q7z6f5 homo sapien

ALIGNMENTS

RESULT 1
ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN Name=TNFRSF17; Synonyms=BCM, BCMA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocytes;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
RA Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
RT by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma";
RL EMBO J. 11:3897-3904(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCMA gene, preferentially expressed during B lymphoid maturation,
RT is bidirectionally transcribed";
RL Nucleic Acids Res. 22:1147-1154(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;
RA Loftus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q";
RL Genomics 60:295-308(1999).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCMA gene: lack of
RT association with systemic lupus erythematosus and rheumatoid
RT arthritis";
RL Genes Immun. 2:276-279(2001).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; ASN-81 AND
RP SER-165.
RA Livingstone R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;

RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RX FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
RA Inoue J.-I., Devesgne O., Teapin A.,
RT "TNF receptor family member BCMA (B cell maturation) associates with
RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
RT activated protein kinase.";
RL J. Immunol. 165:1322-1330(2000).
RN [7]
RX FUNCTION.
RX MEDLINE=20359066; PubMed=10801128; DOI=10.1038/35010115;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
RA Harrison K., Kindsvogel W., Clegg C.H.;
RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
RT autoimmune disease.";
RL Nature 404:995-999(2000).
RN [8]
RX FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Booné T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [9]
RX INTERACTIONS WITH TRAF5 AND TRAF6.
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
RA Shu H.-B., Johnson H.;
RT "B cell maturation protein is a receptor for the tumor necrosis factor
RT family member TALL-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
RN [10]
RX FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK.
CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC and perinuclear Golgi-like structures.
CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC cells or monocytes.
CC -1- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia
CC (T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which
CC involves TNFSF17 and IL2.
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z14954; CAA78679.1; -
DR EMBL; Z29575; CAA82691.1; -
DR EMBL; Z29574; CAA82690.1; -
DR EMBL; U95742; AAB67251.1; -
DR EMBL; AB052772; BAB60895.1; -
DR EMBL; AY509112; AAR84240.1; -
DR FIC; S43486; S43486.
DR PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.
DR Genew; HGNC:11913; TNFRSF17.
DR MIM; 103545; -
DR GO; 0016021; C:integral to membrane; TAS.
DR GO; 0005886; C:plasma membrane; TAS.
DR GO; 0004872; F:receptor activity; TAS.

DR GO; 0008283; P:cell proliferation; TAS.
DR GO; 0007275; P:development; TAS.
DR GO; 0007165; P:signal transduction; TAS.
KW 3D-structure; Chromosomal translocation; Immune response;
KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
FT DOMAIN 1 54 Extracellular (Potential).
FT TRANSMEM 55 77 Signal-anchor for type III membrane
FT protein (Potential).
FT Cytoplasmic (Potential).
FT DOMAIN 78 184 TNFR-Cys.
FT REPEAT 7 4 Breakpoint for translocation to form
FT SITE 3 4 IL2/TNFRSF17 oncogene.
FT DISULFID 8 21 By similarity.
FT DISULFID 24 37 By similarity.
FT DISULFID 28 41 By similarity.
FT VARIANT 54 54 A -> V.
FT VARIANT 65 65 /FTID=VAR_018755.
FT VARIANT 75 75 I -> V.
FT VARIANT 81 81 F -> V.
FT VARIANT 153 153 /FTID=VAR_018757.
FT VARIANT 153 153 /FTID=VAR_018758.
FT VARIANT 165 165 A -> T.
FT VARIANT 165 165 /FTID=VAR_012234.
FT VARIANT 165 165 C -> S.
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;
Query Match 100.0%; Score 283; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLOWAGQCSQNEYFDSLHACIPCLRCSSNTPPLTCORYCNASVTNSVKG 51
DB 1 MLOWAGQCSQNEYFDSLHACIPCLRCSSNTPPLTCORYCNASVTNSVKG 51
RESULT 2
Q8PE46 PRELIMINARY; PRT; 184 AA.
ID Q8PE46
AC Q6PE46;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 17.
GN Name=TNFRSF17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AH58291.1; -;
 KW GO: GO:0004872; F:receptor activity; IEA.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;
 Query Match 100.0%; Score 283; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4e-27;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQWAGCQSQNEFYDLSLHACIPQLRCSSNTPLTCQRYCNASVTSNKG 51
 |||||
 DB 1 MLQWAGCQSQNEFYDLSLHACIPQLRCSSNTPLTCQRYCNASVTSNKG 51
 |||||
 RESULT 3
 TR17 MOUSE STANDARD; PRT; 185 AA.
 ID TR17 MOUSE
 AC C88472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 maturation protein).
 GN Name=TNfrsf17; Synonyms=BCM, BCMA;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 of the tumor necrosis factor receptor superfamily. ";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimonard S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konacaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells G.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs. ";
 Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 Promotes B-cell survival and plays a role in the regulation of
 humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoID=O88472-1; Sequences=Displayed;
 CC Name=2;
 CC IsoID=O88472-2; Sequences=VSP 006507;
 CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 heart, and at lower levels in kidney and lung.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 CC EMBL; AF061505; AAC23799.1; -;
 CC EMBL; AK020247; BAB32038.1; -;
 CC EMBL; BC027519; AAH27519.1; -;
 CC HSSP; Q02223; 1OOP.
 CC MGD; MGI:1343050; Tnftrsf17.
 CC Alternative splicing; Immune response; Receptor; Signal-anchor;
 Transmembrane.
 KW DOMAIN 1 49 Extracellular (Potential).
 FT TRANSMEM 50 70 Signal-anchor for type III membrane
 protein (Potential).
 FT DOMAIN 71 185 Cytoplasmic (Potential).
 FT REPEAT 4 36 TNFR-Cys
 FT DISULFID 5 18 By similarity.
 FT DISULFID 21 32 By similarity.
 FT DISULFID 25 36 By similarity.
 FT VARSPLIC 87 91 Missing (in isoform 2).
 FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;
 SQ
 Query Match 64.0%; Score 181; DB 1; Length 185;
 Best Local Similarity 70.8%; Pred. No. 1.7e-14;

Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPTLCORYCNASVTNSVKG 51
DB 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCYCDPSVTSSVKG 46

RESULT 4
Q9BI07 PRELIMINARY; PRT; 718 AA.
ID Q9BI07;
AC Q9BI07;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative cysteine surface protein (Fragment).
GN Name=csp;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21428166; PubMed=11545438;
RA Willhoelt U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
RT "Introns of Entamoeba histolytica and Entamoeba dispar.";
RL Protist 152:149-156(2001).
DR EMBL: AJ409106; CAC34072.1; -;
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR009030; Grow_fac_recept.
DR SMART; SM00261; FU; 6.
FT NON TER 718 718
SQ SEQUENCE 718 AA; 80231 MW; FFF6362A49F2827A CRC64;

Query Match 25.8%; Score 73; DB 2; Length 718;
Best Local Similarity 26.5%; Pred. No. 1.7;
Matches 13; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

QY 3 OMAGQCSQNEYFDSLHACIPCOLRCSSNTPTLCORYCNASVTNSVKG 51
DB 136 ELICGRCDGSYFDSITRTTQCKFNCELTSSTNCFKSNKILTESNG 184

RESULT 5
O88714 PRELIMINARY; PRT; 499 AA.
ID O88714;
AC O88714;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gastric mucin-like protein (Fragment).
GN Name=Muc6; Synonyms=gastic mucin-like;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Tomasetto C.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -;
DR HSP; P56682; ICCV.
DR MGD; MGI:2663233; Muc6.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00216; VWD; 1.

FT NON TER 1 1
FT NON TER 499 499
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61B CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 499;
Best Local Similarity 48.3%; Pred. No. 1.3;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPTLT 36
DB 430 CSQNEYFDHSEGTVCVC-----APPT 451

RESULT 6
Q80218 PRELIMINARY; PRT; 1674 AA.
ID Q80218;
AC Q80218;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted gel-forming mucin (Fragment).
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX PubMed=14984930; DOI=10.1016/j.bbexp.2004.01.001;
RA Escande F., Buisine M.P.;
RT "The mouse secreted gel-forming mucin gene cluster.";
RL Biochim. Biophys. Acta 1676:240-250(2004).
DR EMBL; AJ511867; CAD54415.1; -;
DR EMBL; AJ511868; CAD54415.1; JOINED.
DR HSP; O46162; IKJ0.
DR MGD; MGI:2663233; Muc6.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR009041; PMP_SSC1.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
FT NON TER 1674 1674
SQ SEQUENCE 1674 AA; 181168 MW; 3BC42CB004476309 CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 1674;
Best Local Similarity 48.3%; Pred. No. 4.6;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPTLT 36
DB 1181 CSQNEYFDHSEGTVCVC-----APPT 1202

RESULT 7
Q80703 PRELIMINARY; PRT; 2850 AA.
ID Q80703;
AC Q80703;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MUC6.
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
RA Desseyn J.-L., Laine A.;

Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLHACIPQLRCSNTPLTCQYVC 41
 Db 6 CPKQYWDSSKSCVSCALTCSQRS-ORTCTDFC 38

RESULT 9
 Q6BFG4

ID Q6BFG4 PRELIMINARY; PRT; 3005 AA.

AC Q6BFG4

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Putative surface protein with EGF domains and furin-like repeats.

GN ORFName=PTMB.409;

OS Paramesitium tetraurelia.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;

OC Paramesitium.

OX NCBI_TaxID=5888;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC STRAIN=Stock d4-2;

RX PubMed=15296759; DOI=10.1016/j.j.cub.2004.07.029;

RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,

RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,

RA Cohen J., Meyer E., Sperling L.,

RT "High Coding Density on the Largest Paramesitium tetraurelia Somatic Chromosome";

RL Curr. Biol. 14:1397-1404 (2004).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Stock d4-2;

RX PubMed=15296759; DOI=10.1016/j.j.cub.2004.07.029;

RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,

RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,

RA Cohen J., Meyer E., Sperling L.,

RT "High Coding Density on the Largest Paramesitium tetraurelia Somatic Chromosome";

RL Curr. Biol. 14:1397-1404 (2004).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Adrenal cortex;

RX MEDLINE=93342056; PubMed=8341687;

RA Lussan J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.,

RT "CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells";

RT Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]

RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.

RX MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;

RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,

RA Bendayan M., Seidah N.G.,

RT "The isoforms of proprotein convertase PC5 are sorted to different subcellular compartments";

RT J. Cell Biol. 135:1261-1275 (1996).

RN [5]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181;

RA Constam D.B., Calton M., Robertson E.J.,

RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis";

RT J. Cell Biol. 134:181-191 (1996).

RN [6]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=97436919; PubMed=9291583;

RX DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;

RA Rancourt S.L., Rancourt D.E.,

RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation";

RT Dev. Genet. 21:75-81 (1997).

CC -!- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

CC -!- SUBCELLULAR LOCATION: PC5A is secreted through the regulated secretory pathway. PC5B is a type I membrane protein localized to a paraneuclear post-Golgi network compartment in communication with early endosomes.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=PC5B; Synonyms=Long;

CC IsoId=004592-1; Sequence=Displayed;

CC Name=PC5A; Synonyms=Short;

CC IsoId=004592-2; Sequence=VSP_005438, VSP_005439;

CC -!- TISSUE SPECIFICITY: PC5A is expressed in most tissues but is most abundant in the intestine and adrenals. PC5B is expressed in the

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).

RC STRAIN=ICR; TISSUE=Intestine;

RX MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O;

RA Nakagawa T., Murakami K., Nakayama K.,

RT "Identification of an isoform with an extremely large Cys-rich region of PC6, a Kex2-like processing endoprotease";

RT FEBS Lett. 327:165-171 (1993).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Brain, and Intestine;

RX MEDLINE=93324489; PubMed=8468318;

RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K., Nakayama K.,

RT "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4";

RT J. Biochem. 113:132-135 (1993).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Adrenal cortex;

RX MEDLINE=93342056; PubMed=8341687;

RA Lussan J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.,

RT "CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells";

RT Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]

RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.

RX MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;

RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K., Bendayan M., Seidah N.G.,

RT "The isoforms of proprotein convertase PC5 are sorted to different subcellular compartments";

RT J. Cell Biol. 135:1261-1275 (1996).

RN [5]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181;

RA Constam D.B., Calton M., Robertson E.J.,

RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis";

RT J. Cell Biol. 134:181-191 (1996).

RN [6]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=97436919; PubMed=9291583;

RX DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;

RA Rancourt S.L., Rancourt D.E.,

RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation";

RT Dev. Genet. 21:75-81 (1997).

CC -!- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

CC -!- SUBCELLULAR LOCATION: PC5A is secreted through the regulated secretory pathway. PC5B is a type I membrane protein localized to a paraneuclear post-Golgi network compartment in communication with early endosomes.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=PC5B; Synonyms=Long;

CC IsoId=004592-1; Sequence=Displayed;

CC Name=PC5A; Synonyms=Short;

CC IsoId=004592-2; Sequence=VSP_005438, VSP_005439;

CC -!- TISSUE SPECIFICITY: PC5A is expressed in most tissues but is most abundant in the intestine and adrenals. PC5B is expressed in the

Query Match 25.1%; Score 71; DB 2; Length 3005;

Best Local Similarity 35.6%; Pred. No. 13;

Matches 16; Conservative 8; Mismatches 11; Indels 10; Gaps 3;

QY 1 MLQMAQQC-SONEYFDSLHACIPQLRCSNTPLTCQ-RCYC 41
 Db 1177 ILKVGNCQCKDGYFESSTNQCICQDLS-FTCQSSKYC 1215

RESULT 10
 PCK5.MOUSE

ID PCK5.MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q62040;

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

DE (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)

DE (Subtilisin-like proprotein convertase 6) (SPC6).

GN Name=Pck5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

FT	ACT_SITE	388	388	Charge relay system (By similarity).
FT	CARBOHYD	227	227	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	383	383	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	667	667	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	754	754	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	804	804	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	854	854	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	951	951	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1016	1016	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1220	1220	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1317	1317	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1523	1523	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1711	1711	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	1733	1733	N-linked (GLNAC. . .) (Potential).
FT	VARSPLIC	878	915	GEYIDQGHGCTCEASCACWGPTEDCISCPVTRVLD -> ATEESNAEGSGFMLVKNNLQCRKVLQQLCKCTCTFG (in isoform PCSA).
FT				/FTid=VSP_005438.
FT	VARSPLIC	916	1877	Missing (in isoform PCSA).
FT				/FTid=VSP_005439.
SEQ	SEQUENCE	1877 AA;	209287 MW;	EC850E2D20BA1C3 CRC64;
	Query Match	24.9%;	Score 70.5;	DB 1; Length 1877;
	Best Local Similarity	34.7%;	Pred. No. 9.2;	Indels 5; Gaps 1;
	Matches	17; Conservative	5; Mismatches	22; Indels 5; Gaps 1;
QY		7	QCSQNEYFSLHLHACIPQLCRCSNTTP-----LTCQRYCNASVTSVK 50	
Db		1480	ECAAVEYWDGSHRCQPCCHKKSCRGSPSEDQCYTCPRETFLNTTCVK 1528	
RESULT 11				
QYR6J7	PRELIMINARY;			
ID	Q7R6J7		PRT;	1025 AA.
AC	Q7R6J7;			
DT	01-MAR-2004	(TEMBLrel. 26, Created)		
DT	01-MAR-2004	(TEMBLrel. 26, Last sequence update)		
DE	01-MAR-2004	(TEMBLrel. 26, Last annotation update)		
DT	GLP 170	141434 144511.		
OS	Giardia lamblia ATCC 50803.			
OC	Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.			
OX	NCBI_Taxid=184922;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WB C6;			
RA	Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,			
RA	Olsen G.J., Sogin M.L.;			
RT	"draft sequence of the Giardia lamblia genome.";			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-! CAUTION: The sequence shown here is derived from an			
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data			
DR	EMBL; AACB01000001; EAA43000.1; --			
DR	HSSP; Q9S7B3; 1EHD.			
DR	InterPro; IPR000345; CytC heme_BS.			
DR	InterPro; IPR009030; Grow fac recept.			
DR	InterPro; IPR020249; Laminin EGF.			
DR	PROSITE; PS001190; CYTOCHROME_C; UNKNOWN 2.			
DR	PROSITE; PS01248; LAMININ TYPE_EGF; UNKNOWN 1.			
SEQ	SEQUENCE	1025 AA;	109044 MW;	36281DF3E2DDB43 CRC64;
	Query Match	24.7%;	Score 70;	DB 2; Length 1025;
	Best Local Similarity	24.2%;	Pred. No. 5.7;	Indels 20; Gaps 2;
	Matches	15; Conservative	8; Mismatches	19; Indels 20; Gaps 2;
QY		4	MAGQCSQNYFSLHLHACIPQLCRCS-----NTPPLTCQRYCNASV 45	
Db		75	ICSSCTDDEVLDLPGFCFSCHSSCTCSGSHFDCLTCRVGELESSPPSACP--CDLQL 132	
QY		46	TN 47	
Db		133	TN 134	

RESULT 12

Q99ND0 PRELIMINARY; PRT; 5374 AA.

AC 099ND0; 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE ZAN (Zonadhesin).

GN Name=Zan;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;

RX MEDLINE=21138439; PubMed=11339002; DOI=10.1093/nar/29.6.1352;

RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,

RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,

RA Miller W., Koop B.F.;

RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human

RT chromosome 7q22 with the orthologous region on mouse chromosome 5.,"

RL Nucleic Acids Res. 29:1352-1365(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;

RX Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;

RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

DR EMBL; AF312033; AAK28824.1; -.

DR EMBL; AY046056; AAL04416.1; -.

DR HSSP; Q90248; 1HX2.

DR MGD; MGI:106656; Zan.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0007339; P:binding of sperm to zona pellucida; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR002919; Cysrich_TIL.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR003645; FOL_N.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR000998; MAM.

DR InterPro; IPR003328; TILA Cysrich.

DR InterPro; IPR001007; VWF_C.

DR InterPro; IPR001846; VWF_D.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00629; MAM; 3.

DR Pfam; PF01826; TIL; 25.

DR Pfam; PF02345; TIL_assoc; 25.

DR Pfam; PF00094; VMD; 4.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00274; FOLN; 20.

DR SMART; SM00137; MAM; 3.

DR SMART; SM00214; VMC; 18.

DR SMART; SM00216; VMD; 4.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 18.

DR PROSITE; PS00266; EGF_3; 1.

DR PROSITE; PS00060; MAM_2; 3.

KW EGF-like domain; Glycoprotein.

SQ SEQUENCE 5374 AA; 579545 MW; 90D2D8CFE5DE24EB CRC64;

Query Match 24.6%; Score 69.5; DB 2; Length 5374;

Best Local Similarity 36.8%; Pred. No. 36;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 7 QCSQNEYFDLSLHACIP-CQLRCSNTP--PLTCQRYC 41

Db 3297 QCTNSQFTDCLPSCVPCSNCEVTSTSVPSCSREGC 3334

RESULT 13

ZAN_MOUSE

ID ZAN_MOUSE STANDARD; PRT; 5376 AA.

AC O88799; O08647;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Zonadhesin precursor.

GN Name=Zan;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415;

RA Gao Z., Garbers D.L.;

RT "Species diversity in the structure of zonadhesin, a sperm-specific

RT membrane protein containing multiple cell adhesion molecule-like

RT domains.,"

RL J. Biol. Chem. 273:3415-3421(1998).

RN [2]

RP SEQUENCE OF 4864-5376 FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;

RA Gao Z., Harumi T., Garbers D.L.;

RT "Chromosome localization of the mouse zonadhesin gene and the human

RT zonadhesin gene (ZAN).,"

RL Genomics 41:119-122(1997).

CC -1- FUNCTION: Birds in a species-specific manner to the zona pellucida

CC of the egg. May be involved in gamete recognition and/or

CC signaling.

CC -1- SUBUNIT: Probably forms covalent oligomers.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the

CC apical region of the sperm head.

CC -1- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.

CC -1- DOMAIN: The MAM domains probably mediates sperm adhesion to the

CC zona pellucida.

CC -1- DOMAIN: During sperm migration through the reproductive tracts,

CC the mucin-like domain might inhibit inappropriate trapping of

CC spermatozoa or promoting adhesion to the oviductal isthmus.

CC -1- DOMAIN: The VWF domain 2 may mediate covalent oligomerization (By

CC similarity).

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 3 MAM domains.

CC -1- SIMILARITY: Contains 25 VWF domains.

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or send an email to license@isb-sib.ch.

EMBL; U97068; AAC26680.1; -.

EMBL; U83190; AAC53125.1; -.

PIR; T42215; T42215.

HSSP; Q90248; 1HX2.

MGD; MGI:106656; Zan.

InterPro; IPR002919; Cysrich_TIL.

InterPro; IPR000742; EGF_2.

InterPro; IPR006209; EGF_like.

InterPro; IPR000998; MAM.

InterPro; IPR003328; TILA Cysrich.

InterPro; IPR001846; VWF_D.

Pfam; PF00008; EGF; 1.

Pfam; PF00629; MAM; 3.

Pfam; PF01826; TIL; 25.

Pfam; PF02345; TIL_assoc; 25.

Pfam; PF00094; VMD; 4.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 18.

```

FT CARBOHYD 4586 4586 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 5136 5136 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 5252 5252 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB77DF2A2620 CRC64;

Query Match 24.6%; Score 69.5; DB 1; Length 5376;
Best Local Similarity 36.8%; Pred.No.36;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 0

Qy 7 QCSONEYFDSLHACIP-CQLRCSNTP--PLTCORYC 41
Db 3299 QPETSQFDCLPSCVPCSNRCEVTSPVPSSCRECC 3336
||| | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |

RESULT 14
ID Q22378 PRELIMINARY; PRT; 966 AA.
AC Q22378;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Tl0E10.4.
GN OXPNames=Tl0E10.4, Tl0E10.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Pelodetrinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium." ;
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Geisel C.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: U39644; AAA80360.2; -.
DR PIR: Tl6840; Tl6840.
DR HSP; P10969; LWGT.
DR WormBase; WBGene00020421; Tl0E10.4.
DR WormPep; Tl0E10.4; CE25989.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_perA.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR003571; Snake toxin.
DR InterPro; IPR006150; Worm_Repeat_1.
DR Pfam; PF01607; CBW_14; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00289; WR1; 12.
DR PROSITE; PS00606; B_KETOACYL SYNTHASE; UNKNOWN 1.

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DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 966 AA, 102460 MW, B565A3CDD25216D9 CRC64;
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Best Local Similarity 36.2%; Pred. No. 8.2;
Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;

QY 7 QCSQNEYFDLSLHACIPQLR--CSNTPTPLTCQRCYNASVTNSVKG 51
Db 215 QCSQSTVFNSDLNVCVPLAIONSCDSSTQOPVCS--C-SQVSSSCPG 258

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ID Q6W4X9 PRELIMINARY; PRT; 1569 AA.
AC Q6W4X9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mucin glycoprotein (Fragment).
GN Names=MUC6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;
RA Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
RA Toribara N.W.;
RT "The complete genomic organization of the human MUC6 and MUC2 mucin
genes";
RL Genomics 83:936-939(2004).
DR EMBL; AY312160; AAQ82434.1; -.
DR InterPro; IPR002919; Cysrich Til.
DR InterPro; IPR009041; PMP_SGGI.
DR InterPro; IPR006552; VWC_out.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00215; VWC_out; 2.
DR SMART; SM00216; VWD; 3.
FT NON_TER 1569 1569
SQ SEQUENCE 1569 AA; 168065 MW; 6AEDEE143ECB855B CRC64;

Query Match 24.2%; Score 68.5; DB 2; Length 1569;
Best Local Similarity 45.2%; Pred. No. 14;
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDLSLHACIPQLRCSNTPTPLTCQ 38
Db 1179 CSQDEYFDHEGVGVPCM-----PPTTPQ 1202

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Job time : 51.0468 secs
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